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OM protein - protein search, using sw model

Run on: March 18, 2004, 07:17:04 ; Search time 33.5 Seconds
(without alignments)
77,300 Million cell updates/sec

Title: US-09-909-348-1
Perfect score: 59
Sequence: 1 CEGDSGGPFV 10

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1049977 seqs, 258955339 residues

Total number of hits satisfying chosen parameters: 32147

Minimum DB seq length: 10
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:

- 1: /cgn2_6/prodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/prodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/prodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/prodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/prodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/prodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/prodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/prodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/prodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/prodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/prodata/1/pubpaa/US09D_PUBCOMB.pep.*
- 13: /cgn2_6/prodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/prodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/prodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/prodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/prodata/1/pubpaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/prodata/1/pubpaa/US10F_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	59	100.0	10	9	US-09-909-348-1
2	59	100.0	10	9	US-09-909-122-1
3	59	100.0	10	13	US-10-050-692-1
4	59	100.0	10	13	US-10-050-688-1
5	46	78.0	10	9	US-09-909-348-2
6	46	78.0	10	9	US-09-909-122-2
7	46	78.0	10	13	US-10-050-692-2
8	46	78.0	10	13	US-10-050-688-2
9	34	57.6	10	10	US-09-572-404B-606
10	28	47.5	10	10	US-09-572-404B-3584
11	27	45.8	10	10	US-09-572-404B-3784
12	27	45.8	10	10	US-09-572-404B-3785
13	25	42.4	10	9	US-09-879-957-55
14	25	42.4	10	10	US-09-572-404B-51
15	25	42.4	10	10	US-09-572-404B-53

16	25	42.4	10	10	US-09-572-404B-55	Sequence 55, Appl
17	25	42.4	10	10	US-09-572-404B-63	Sequence 63, Appl
18	25	42.4	10	10	US-09-572-404B-174	Sequence 174, App
19	25	42.4	10	10	US-09-572-404B-2027	Sequence 2027, Ap
20	25	42.4	10	10	US-09-572-404B-2033	Sequence 2033, Ap
21	25	42.4	10	10	US-09-572-404B-2091	Sequence 2091, Ap
22	25	42.4	10	10	US-09-572-404B-2093	Sequence 2093, Ap
23	25	42.4	10	10	US-09-572-404B-2095	Sequence 2095, Ap
24	25	42.4	10	10	US-09-572-404B-2798	Sequence 2798, Ap
25	25	42.4	10	10	US-09-572-404B-2798	Sequence 319, App
26	25	42.4	10	10	US-09-932-165-319	Sequence 532, App
27	25	42.4	10	10	US-09-932-165-532	Sequence 745, App
28	25	42.4	10	10	US-09-932-165-745	Sequence 928, App
29	25	42.4	10	10	US-09-932-165-928	Sequence 1084, Ap
30	24	40.7	10	9	US-09-765-086-58	Sequence 58, Appl
31	24	40.7	10	10	US-09-572-404B-4	Sequence 4, Appl1
32	24	40.7	10	10	US-09-572-270A-277	Sequence 277, App
33	24	40.7	10	10	US-09-572-270A-281	Sequence 281, App
34	24	40.7	10	10	US-09-572-270A-283	Sequence 283, App
35	24	40.7	10	10	US-09-572-270A-285	Sequence 285, App
36	24	40.7	10	10	US-09-572-270A-293	Sequence 293, App
37	24	40.7	10	10	US-09-572-270A-295	Sequence 295, App
38	24	40.7	10	13	US-10-008-355-25	Sequence 25, Appl
39	24	40.7	10	14	US-10-264-374-58	Sequence 58, Appl
40	24	40.7	10	14	US-10-375-992-58	Sequence 58, Appl
41	23	39.0	10	10	US-09-572-404B-114	Sequence 114, App
42	23	39.0	10	10	US-09-572-404B-176	Sequence 176, App
43	23	39.0	10	10	US-09-572-404B-342	Sequence 342, App
44	23	39.0	10	10	US-09-572-404B-344	Sequence 344, App
45	23	39.0	10	10	US-09-572-404B-1306	Sequence 1306, Ap

ALIGNMENTS

RESULT 1
US-09-909-348-1
; Sequence 1, Application US/09909348
; Patent No. US20020042373A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; APPLICANT: Crowther, Roger S.
; APPLICANT: Stierberg, Janet
; APPLICANT: Bergmann, John
; TITLE OF INVENTION: Stimulation Of Cartilage Growth With Agonists
; FILE REFERENCE: 3033.1003-001
; CURRENT APPLICATION NUMBER: US/09/909,348
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 607219,800
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide fragment of Thrombin
US-09-909-348-1

Query Match 100.0%; Score 59; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0076;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 CEGDSGGPFV 10

Db 1 CEGDSGGPFV 10

RESULT 2

US-09-909-122-1
; Sequence 1, Application US/09909122

Appl.

Patent No. US20020128202A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; APPLICANT: Crowther, Roger S.
; APPLICANT: Simmons, David J.
; APPLICANT: Yang, Jinping
; APPLICANT: Redin, William R.
; TITLE OF INVENTION: Stimulation Of Bone Growth With Thrombin
; FILE OF INVENTION: Peptide Derivatives
; FILE REFERENCE: 3033.1002-001
; CURRENT APPLICATION NUMBER: US/09/909,122
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/219,300
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide fragment of Thrombin
US-09-909-122-1

Query Match 100.0%; Score 59; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0076;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CEGDSGGPFV 10
Db 1 CEGDSGGPFV 10

RESULT 3

US-10-050-692-1
; Sequence 1, Application US/10050692
; Publication No. US20020182205A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; APPLICANT: Crowther, Roger S.
; APPLICANT: Simmons, David J.
; APPLICANT: Yang, Jinping
; APPLICANT: Redin, William R.
; TITLE OF INVENTION: STIMULATION OF BONE GROWTH WITH THROMBIN
; FILE OF INVENTION: PEPTIDE DERIVATIVES
; FILE REFERENCE: 3033.1002-004
; CURRENT APPLICATION NUMBER: US/10/050,692
; CURRENT FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: 09/909,122
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/219,300
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fragment of human prothrombin
US-10-050-692-1

Query Match 100.0%; Score 59; DB 13; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0076;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CEGDSGGPFV 10
Db 1 CEGDSGGPFV 10

RESULT 4

US-10-050-688-1

Sequence 1, Application US/10050688
; Publication No. US20020198154A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; APPLICANT: Crowther, Roger S.
; APPLICANT: Stierberg, Janet
; APPLICANT: Bergmann, John
; TITLE OF INVENTION: STIMULATION OF CARTILAGE GROWTH WITH
; TITLE OF INVENTION: AGONISTS OF THE NON-PROTEOLYTICALLY ACTIVATED THROMBIN
; FILE OF INVENTION: RECEPTOR
; FILE REFERENCE: 3033.1003-004
; CURRENT APPLICATION NUMBER: US/10/050,688
; CURRENT FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: 09/909,348
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/219,800
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide fragment of thrombin
US-10-050-688-1

Query Match 100.0%; Score 59; DB 13; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0076;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CEGDSGGPFV 10
Db 1 CEGDSGGPFV 10

RESULT 5

US-09-909-348-2
; Sequence 2, Application US/09909348
; Patent No. US20020042373A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; APPLICANT: Crowther, Roger S.
; APPLICANT: Stierberg, Janet
; APPLICANT: Bergmann, John
; TITLE OF INVENTION: Stimulation Of Cartilage Growth With Agonists
; TITLE OF INVENTION: Of The No. US20020042373A1-Proteolytically Activated Thrombin Re
; FILE REFERENCE: 3033.1003-001
; CURRENT APPLICATION NUMBER: US/09/909,348
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/219,800
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide fragment of Thrombin
; NAME/KEY: VARIANT
; LOCATION: (1)...(10)
; OTHER INFORMATION: Xaa at position two is Glu or Gln
; OTHER INFORMATION: Xaa at position nine is Phe, Met, Leu, His or Val
US-09-909-348-2

Query Match 78.0%; Score 46; DB 9; Length 10;
Best Local Similarity 80.0%; Pred. No. 0.83;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CEGDSGGPFV 10
Db 1 CEGDSGGPFV 10

```
RESULT 6
US-09-909-122-2
; Sequence 2, Application US/09909122
; Patent No. US20020128202A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; APPLICANT: Crowther, Roger S.
; APPLICANT: Simmons, David J.
; APPLICANT: Yang, Jinping
; APPLICANT: Redin, William R.
; TITLE OF INVENTION: Stimulation Of Bone Growth With Thrombin
; TITLE OF INVENTION: Peptide Derivatives
; FILE REFERENCE: 3033.1002-001
; CURRENT APPLICATION NUMBER: US/09/909,122
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/219,300
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 10
; TYPE: PPT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide fragment of Thrombin
; NAME/KEY: VARIANT
; LOCATION: (1)...(10)
; OTHER INFORMATION: Xaa at position two is Glu or Gln
; OTHER INFORMATION: Xaa at position nine is Phe, Met, Leu, His or Val
US-09-909-122-2

Query Match      78.0%; Score 46; DB 9; Length 10;
Best Local Similarity 80.0%; Pred. No. 0.83;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CEGDSGGPFV 10
DB      1 CXGDSGGPFV 10

RESULT 7
US-10-050-692-2
; Sequence 2, Application US/10050692
; Publication No. US20020182205A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; APPLICANT: Crowther, Roger S.
; APPLICANT: Simmons, David J.
; APPLICANT: Yang, Jinping
; APPLICANT: Redin, William R.
; TITLE OF INVENTION: STIMULATION OF BONE GROWTH WITH THROMBIN
; TITLE OF INVENTION: PEPTIDE DERIVATIVES
; FILE REFERENCE: 3033.1002-004
; CURRENT APPLICATION NUMBER: US/10/050,692
; CURRENT FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: 09/909,122
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/219,300
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 10
; TYPE: PPT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human fragment of prothrombin
; NAME/KEY: VARIANT
; LOCATION: (2)...(2)
; OTHER INFORMATION: Xaa = Glu or Gln
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; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (9)...(9)
; OTHER INFORMATION: Xaa = Phe, Met, Leu, His or Val
US-10-050-692-2

Query Match      78.0%; Score 46; DB 13; Length 10;
Best Local Similarity 80.0%; Pred. No. 0.83;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CEGDSGGPFV 10
DB      1 CXGDSGGPFV 10

RESULT 8
US-10-050-688-2
; Sequence 2, Application US/10050688
; Publication No. US20020198154A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; APPLICANT: Crowther, Roger S.
; APPLICANT: Stierberg, Janet
; APPLICANT: Bergmann, John
; TITLE OF INVENTION: STIMULATION OF CARTILAGE GROWTH WITH
; TITLE OF INVENTION: AGONISTS OF THE NON-PROTEOLYTICALLY ACTIVATED THROMBIN
; TITLE OF INVENTION: RECEPTOR
; FILE REFERENCE: 3033.1003-004
; CURRENT APPLICATION NUMBER: US/10/050,688
; CURRENT FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: 09/909,348
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/219,800
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 10
; TYPE: PPT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide fragment of thrombin
; NAME/KEY: VARIANT
; LOCATION: (2)...(2)
; OTHER INFORMATION: Xaa = Glu or Gln
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (9)...(9)
; OTHER INFORMATION: Xaa = Phe, Met, Leu, His or Val
US-10-050-688-2

Query Match      78.0%; Score 46; DB 13; Length 10;
Best Local Similarity 80.0%; Pred. No. 0.83;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CEGDSGGPFV 10
DB      1 CXGDSGGPFV 10

RESULT 9
US-09-572-404B-606
; Sequence 606, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: Protpatent version 1.0
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; SEQ ID NO 606
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:

; OTHER INFORMATION: sequence located in C2 at 674-683 and may interact with Sequence
; OTHER INFORMATION: this patent.
US-09-572-404B-606

Query Match 57.6%; Score 34; DB 10; Length 10;
Best Local Similarity 71.4%; Pred. No. 63;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CEGDSGG 7
|:|:|:|
Db 2 CKGESGG 8

RESULT 10

US-09-572-404B-3584
; Sequence 3584, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:

; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 3584
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:

; OTHER INFORMATION: sequence located in PXR1 OR PEX5 at 811-820 and may interact with
; OTHER INFORMATION: Sequence 3583 in this patent.
US-09-572-404B-3584

Query Match 47.5%; Score 28; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GDSGG 7
|:|:|:|
Db 6 GDSGG 10

RESULT 11

US-09-572-404B-3784
; Sequence 3784, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:

; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 3784
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:

; OTHER INFORMATION: sequence located in ERK5 OR ERK4 at 543-552 and may interact with
; OTHER INFORMATION: Sequence 3785 in this patent.
US-09-572-404B-3784

Query Match 45.8%; Score 27; DB 10; Length 10;
Best Local Similarity 83.3%; Pred. No. 7.8e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GDSGGP 8
|:|:|:|
Db 3 GASGGP 8

RESULT 12

US-09-572-404B-3785
; Sequence 3785, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:

; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 3785
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:

; OTHER INFORMATION: sequence located in ERK5 OR ERK4 at 543-552 and may interact with
; OTHER INFORMATION: Sequence 3784 in this patent.
US-09-572-404B-3785

Query Match 45.8%; Score 27; DB 10; Length 10;
Best Local Similarity 83.3%; Pred. No. 7.8e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GDSGGP 8
|:|:|:|
Db 3 GASGGP 8

RESULT 13

US-09-879-957-55
; Sequence 55, Application US/09879957
; Patent No. US20020034755A1
; GENERAL INFORMATION:

; APPLICANT: SPARKS, Andrew B.
; HOFFMAN, No. US20020034755A1h
; KAY, Brian K.
; FOWLKES, Dana M.
; MCCONNELL, Stephen J.

; TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
; DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
; USING SAME

; NUMBER OF SEQUENCES: 227

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA

; ZIP: 10036-2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/879,957

; FILING DATE: 13-Jun-2001

; CLASSIFICATION: <unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/630,915

; FILING DATE: 03-APR-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Misrock, S. Leslie

; REGISTRATION NUMBER: 18,872

; REFERENCE/DOCKET NUMBER: 1101-174

; TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Other
LOCATION: 8
OTHER INFORMATION: Undefined
SEQUENCE DESCRIPTION: SEQ ID NO: 55:
US-09-879-957-55

Query Match 42.4%; Score 25; DB 9; Length 10;
Best Local Similarity 71.4%; Pred. No. 1.6e+03;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CEGDSGG 7
Db 1 CMGDSLG 7

RESULT 14
US-09-572-404B-51
; Sequence 51, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human Patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 51
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in CBFA2 OR AML1 at 360-369 and may interact with
; OTHER INFORMATION: Sequence 52 in this patent.
US-09-572-404B-51

Query Match 42.4%; Score 25; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GGPF 9
Db 7 GGPF 10

RESULT 15
US-09-572-404B-53
; Sequence 53, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human Patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 53
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:

Query Match 42.4%; Score 25; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GGPF 9
Db 7 GGPF 10

Search completed: March 18, 2004, 07:26:10
Job time : 33.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 18, 2004, 07:16:14 ; Search time 26.1905 Seconds
(without alignments)
98.874 Million cell updates/sec

Title: US-09-909-348-1
Perfect score: 59
Sequence: 1 CEGDSGGPFV 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1049977 seqs, 25995339 residues

Total number of hits satisfying chosen parameters: 1049977

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US08A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US08B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	59	100.0	10	9	US-09-909-348-1
2	59	100.0	10	9	US-09-909-122-1
3	59	100.0	10	13	US-10-050-692-1
4	59	100.0	10	13	US-10-050-688-1
5	59	100.0	12	9	US-09-904-090-2
6	59	100.0	12	13	US-10-050-611-2
7	59	100.0	23	9	US-09-777-328-8
8	59	100.0	23	9	US-09-904-090-3
9	59	100.0	23	13	US-10-050-692-6
10	59	100.0	23	13	US-10-050-611-3
11	59	100.0	23	13	US-10-050-611-4
12	59	100.0	23	13	US-10-050-688-5
13	59	100.0	23	13	US-10-050-688-6
14	59	100.0	25	9	US-09-909-348-5
15	59	100.0	25	9	US-09-909-122-5

16	59	100.0	25	13	US-10-050-692-5	Sequence 5, Appli
17	59	100.0	250	10	US-09-898-837A-45	Sequence 45, Appl
18	59	100.0	251	10	US-09-898-837A-41	Sequence 41, Appl
19	59	100.0	259	15	US-10-165-442-2	Sequence 2, Appli
20	59	100.0	259	15	US-10-165-442-4	Sequence 4, Appli
21	59	100.0	295	15	US-10-165-442-1	Sequence 1, Appli
22	59	100.0	295	15	US-10-165-442-3	Sequence 3, Appli
23	59	100.0	622	14	US-10-020-141-8	Sequence 8, Appli
24	59	100.0	622	14	US-10-017-631-2	Sequence 2, Appli
25	59	100.0	622	14	US-10-214-932-116	Sequence 116, App
26	59	100.0	622	14	US-10-172-712-29	Sequence 29, Appl
27	56	94.9	164	14	US-10-357-175-25	Sequence 25, Appl
28	56	94.9	164	15	US-10-455-720-25	Sequence 25, Appl
29	56	94.9	304	10	US-09-898-837A-44	Sequence 44, Appl
30	56	94.9	304	15	US-10-099-322-139	Sequence 139, App
31	56	94.9	304	15	US-10-044-564-139	Sequence 139, App
32	56	94.9	305	15	US-10-108-260A-3002	Sequence 3002, Ap
33	56	94.9	376	9	US-09-820-002-2	Sequence 2, Appli
34	56	94.9	376	14	US-10-374-031-2	Sequence 2, Appli
35	56	94.9	380	12	US-10-235-789-2	Sequence 2, Appli
36	56	94.9	416	15	US-10-099-322-138	Sequence 138, App
37	56	94.9	416	15	US-10-044-564-138	Sequence 138, App
38	56	94.9	417	9	US-09-820-002-4	Sequence 4, Appli
39	56	94.9	417	10	US-09-776-191-68	Sequence 68, Appl
40	56	94.9	417	14	US-10-073-060-2	Sequence 2, Appli
41	56	94.9	417	14	US-10-205-823-178	Sequence 178, App
42	56	94.9	417	14	US-10-374-031-4	Sequence 4, Appli
43	56	94.9	417	15	US-10-099-322-40	Sequence 40, Appl
44	56	94.9	417	15	US-10-099-322-136	Sequence 136, App
45	56	94.9	417	15	US-10-295-027-1377	Sequence 1377, Ap

ALIGNMENTS

RESULT 1

US-09-909-348-1
; Sequence 1, Application US/09909348
; Patent No. US20020042373A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; APPLICANT: Crowther, Roger S.
; APPLICANT: Stierberg, Janet
; APPLICANT: Bergmann, John
; TITLE OF INVENTION: Stimulation Of Cartilage Growth With Agonists
; FILE OF INVENTION: Of The No. US20020042373A1-Proteolytically Activated Thrombin Re
; FILE REFERENCE: 3033.1003-001
; CURRENT APPLICATION NUMBER: US/09/909,348
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/219,800
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Peptide fragment of Thrombin
US-09-909-348-1

Query Match 100.0%; Score 59; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0076;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CEGDSGGPFV 10
Db 1 CEGDSGGPFV 10

RESULT 2
US-09-909-122-1
; Sequence 1, Application US/09909122

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; Patent No. US20020128202A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; APPLICANT: Crowther, Roger S.
; APPLICANT: Simmons, David J.
; APPLICANT: Yang, Jiping
; APPLICANT: Redin, William R.
; TITLE OF INVENTION: Stimulation Of Bone Growth With Thrombin
; TITLE OF INVENTION: Peptide Derivatives
; FILE REFERENCE: 3033.1002-001
; CURRENT APPLICATION NUMBER: US/09/909,122
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/219,300
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide fragment of Thrombin
US-09-909-122-1

Query Match 100.0%; Score 59; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0076;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CEGDSGGPFV 10
Db 1 CEGDSGGPFV 10

RESULT 3
US-10-050-692-1
; Sequence 1, Application US/10050692
; Publication No. US20020182205A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; APPLICANT: Crowther, Roger S.
; APPLICANT: Simmons, David J.
; APPLICANT: Yang, Jiping
; APPLICANT: Redin, William R.
; TITLE OF INVENTION: STIMULATION OF BONE GROWTH WITH THROMBIN
; TITLE OF INVENTION: PEPTIDE DERIVATIVES
; FILE REFERENCE: 3033.1002-004
; CURRENT APPLICATION NUMBER: US/10/050,692
; CURRENT FILING DATE: 2002-01-16
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 09/909,122
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/219,300
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fragment of human prothrombin
US-10-050-692-1

Query Match 100.0%; Score 59; DB 13; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0076;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CEGDSGGPFV 10
Db 1 CEGDSGGPFV 10

RESULT 4
US-10-050-688-1

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; Sequence 1, Application US/10050688
; Publication No. US20020198154A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; APPLICANT: Crowther, Roger S.
; APPLICANT: Stierberg, Janet
; APPLICANT: Bergmann, John
; TITLE OF INVENTION: STIMULATION OF CARTILAGE GROWTH WITH
; TITLE OF INVENTION: AGONISTS OF THE NON-PROTEOLYTICALLY ACTIVATED THROMBIN
; TITLE OF INVENTION: RECEPTOR
; FILE REFERENCE: 3033.1003-004
; CURRENT APPLICATION NUMBER: US/10/050,688
; CURRENT FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: 09/909,348
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/219,800
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide fragment of thrombin
US-10-050-688-1

Query Match 100.0%; Score 59; DB 13; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0076;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CEGDSGGPFV 10
Db 1 CEGDSGGPFV 10

RESULT 5
US-09-904-090-2
; Sequence 2, Application US/09904090
; Patent No. US20020061852A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell
; TITLE OF INVENTION: METHODS OF THERAPY WITH THROMBIN DERIVED
; TITLE OF INVENTION: PEPTIDES
; FILE REFERENCE: 3033.1000-001
; CURRENT APPLICATION NUMBER: US/09/904,090
; CURRENT FILING DATE: 2001-07-12
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/217,583
; PRIOR FILING DATE: 2000-07-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide, fragment of thrombin
US-09-904-090-2

Query Match 100.0%; Score 59; DB 9; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0091;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CEGDSGGPFV 10
Db 3 CEGDSGGPFV 12

RESULT 6
US-10-050-611-2
; Sequence 2, Application US/10050611
; Publication No. US20020187933A1
; GENERAL INFORMATION:

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; APPLICANT: Carney, Darrell H.
; TITLE OF INVENTION: METHODS OF THERAPY WITH THROMBIN DERIVED
; FILE REFERENCE: 3033.1000-008
; CURRENT APPLICATION NUMBER: US/10/050,611
; PRIOR FILING DATE: 2002-01-16
; PRIOR FILING DATE: 2001-07-12
; PRIOR FILING DATE: 2000-07-12
; PRIOR FILING DATE: 2000-07-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human fragment of thrombin
US-10-050-611-2

Query Match 100.0%; Score 59; DB 13; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0091;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CEGDSGGPFV 10
Db 3 CEGDSGGPFV 12

RESULT 7
US-09-777-328-8
; Sequence 8, Application US/09777328
; Patent No. US20020032314A1
; GENERAL INFORMATION:
; APPLICANT: CAREY, DARRELL H.
; APPLICANT: RAMAKRISHNAN, SHYAM
; TITLE OF INVENTION: SYNTHETIC PEPTIDE NEUTROPHIL CELL CHEMOTACTIC AGENTS
; FILE REFERENCE: CHBP:002
; CURRENT APPLICATION NUMBER: US/09/777,328
; CURRENT FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 08/330,594
; PRIOR FILING DATE: 1994-10-28
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-777-328-8

Query Match 100.0%; Score 59; DB 9; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CEGDSGGPFV 10
Db 14 CEGDSGGPFV 23

RESULT 8
US-09-904-090-3
; Sequence 3, Application US/09904090
; Patent No. US20020061852A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell
; TITLE OF INVENTION: METHODS OF THERAPY WITH THROMBIN DERIVED
; FILE REFERENCE: 3033.1000-001
; CURRENT APPLICATION NUMBER: US/09/904,090
; CURRENT FILING DATE: 2001-07-12

; PRIOR APPLICATION NUMBER: US 60/217,583
; PRIOR FILING DATE: 2000-07-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide, fragment of thrombin
US-09-904-090-3

Query Match 100.0%; Score 59; DB 9; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CEGDSGGPFV 10
Db 14 CEGDSGGPFV 23

RESULT 9
US-10-050-692-6
; Sequence 6, Application US/10050692
; Publication No. US20020182205A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; APPLICANT: Crowther, Roger S.
; APPLICANT: Simmons, David J.
; APPLICANT: Yang, Jinding
; APPLICANT: Redin, William R.
; TITLE OF INVENTION: STIMULATION OF BONE GROWTH WITH THROMBIN
; FILE REFERENCE: 3033.1002-004
; CURRENT APPLICATION NUMBER: US/10/050,692
; CURRENT FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: 09/909,122
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/219,300
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: c-terminal amidated fragment of human thrombin
; OTHER INFORMATION: valine is amidated as CONH2
US-10-050-692-6

Query Match 100.0%; Score 59; DB 13; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CEGDSGGPFV 10
Db 14 CEGDSGGPFV 23

RESULT 10
US-10-050-611-3
; Sequence 3, Application US/10050611
; Publication No. US20020187933A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; TITLE OF INVENTION: METHODS OF THERAPY WITH THROMBIN DERIVED
; FILE REFERENCE: 3033.1000-008
; CURRENT APPLICATION NUMBER: US/10/050,611

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; CURRENT FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: 09/904,090
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 60/217,583
; PRIOR FILING DATE: 2000-07-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human fragment of thrombin
US-10-050-611-3

Query Match 100.0%; Score 59; DB 13; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CEGDSGGPFV 10
Db 14 CEGDSGGPFV 23

RESULT 11
US-10-050-611-4
; Sequence 4, Application US/10050611
; Publication No. US20020187933A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; TITLE OF INVENTION: METHODS OF THERAPY WITH THROMBIN DERIVED
; TITLE OF INVENTION: PEPTIDES
; FILE REFERENCE: 3033.1000-008
; CURRENT APPLICATION NUMBER: US/10/050,611
; CURRENT FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: 09/904,090
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 60/217,583
; PRIOR FILING DATE: 2000-07-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: c-terminal amidated fragment of human thrombin
; FEATURE:
; NAME/KEY: AMIDATION
; LOCATION: 23
; OTHER INFORMATION: valine is amidated as CONH2
US-10-050-611-4

Query Match 100.0%; Score 59; DB 13; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CEGDSGGPFV 10
Db 14 CEGDSGGPFV 23

RESULT 12
US-10-050-688-5
; Sequence 5, Application US/10050688
; Publication No. US20020198154A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; APPLICANT: Crowther, Roger S.
; APPLICANT: Stierberg, Janet
; APPLICANT: Bergmann, John
; TITLE OF INVENTION: STIMULATION OF CARTILAGE GROWTH WITH
; AGONISTS OF THE NON-PROTEOLYTICALLY ACTIVATED THROMBIN
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; TITLE OF INVENTION: RECEPTOR
; FILE REFERENCE: 3033.1003-004
; CURRENT APPLICATION NUMBER: US/10/050,688
; CURRENT FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: 09/909,348
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/219,800
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide fragment of thrombin
US-10-050-688-5

Query Match 100.0%; Score 59; DB 13; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CEGDSGGPFV 10
Db 14 CEGDSGGPFV 23

RESULT 13
US-10-050-688-6
; Sequence 6, Application US/10050688
; Publication No. US20020198154A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; APPLICANT: Crowther, Roger S.
; APPLICANT: Stierberg, Janet
; APPLICANT: Bergmann, John
; TITLE OF INVENTION: AGONISTS OF THE NON-PROTEOLYTICALLY ACTIVATED THROMBIN
; TITLE OF INVENTION: RECEPTOR
; FILE REFERENCE: 3033.1003-004
; CURRENT APPLICATION NUMBER: US/10/050,688
; CURRENT FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: 09/909,348
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/219,800
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide fragment of thrombin
; FEATURE:
; NAME/KEY: AMIDATION
; LOCATION: (23)---(23)
; OTHER INFORMATION: CONH2
US-10-050-688-6

Query Match 100.0%; Score 59; DB 13; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CEGDSGGPFV 10
Db 14 CEGDSGGPFV 23

RESULT 14
US-09-909-348-5
; Sequence 5, Application US/09909348
; Patent No. US20020042373A1
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; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; APPLICANT: Crowther, Roger S.
; APPLICANT: Stierberg, Janet
; APPLICANT: Bergmann, John
; TITLE OF INVENTION: Stimulation Of Cartilage Growth With Agonists
; TITLE OF INVENTION: Of The No. US2002004237A1-Proteolytically Activated Thrombin Re
; FILE REFERENCE: 3033.1003-001
; CURRENT APPLICATION NUMBER: US/09/909,348
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/219,800
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide fragment of Thrombin
US-09-909-348-5

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Query Match 100.0%; Score 59; DB 9; Length 25;
Best Local Similarity 100.0%; Pred.No. 0.018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 CEGDSGGPFV 10
Db 16 CEGDSGGPFV 25

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RESULT 15

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US-09-909-122-5
; Sequence 5, Application US/09909122
; Patent No. US20020128202A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; APPLICANT: Crowther, Roger S.
; APPLICANT: Simmons, David J.
; APPLICANT: Yang, Jiping
; APPLICANT: Redin, William R.
; TITLE OF INVENTION: Stimulation Of Bone Growth With Thrombin
; TITLE OF INVENTION: Peptide Derivatives
; FILE REFERENCE: 3033.1002-001
; CURRENT APPLICATION NUMBER: US/09/909,122
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/219,300
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide fragment of Thrombin
US-09-909-122-5

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Query Match 100.0%; Score 59; DB 9; Length 25;
Best Local Similarity 100.0%; Pred.No. 0.018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 CEGDSGGPFV 10
Db 16 CEGDSGGPFV 25

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Search completed: March 18, 2004, 07:24:51
Job time : 27.1905 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 18, 2004, 07:17:04 ; Search time 33.5 Seconds
(without alignments)
77.300 Million cell updates/sec

Title: US-09-909-348-2

Perfect score: 50

Sequence: 1 CXGDSGGPXY 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1049977 seqs, 258955339 residues

Total number of hits satisfying chosen parameters: 32147

Minimum DB seq length: 10

Maximum DB seq length: 10

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

- 1: /cgn2_6/prodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/prodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/prodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/prodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/prodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/prodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/prodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/prodata/1/pubpaa/US08A_PUBCOMB.pep.*
- 10: /cgn2_6/prodata/1/pubpaa/US08B_PUBCOMB.pep.*
- 11: /cgn2_6/prodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/prodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/prodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/prodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/prodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/prodata/1/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/prodata/1/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/prodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	92.0	10	9	US-09-909-348-1
2	46	92.0	10	9	US-09-909-348-2
3	46	92.0	10	9	US-09-909-122-1
4	46	92.0	10	9	US-09-909-122-2
5	46	92.0	10	13	US-10-050-692-1
6	46	92.0	10	13	US-10-050-692-2
7	46	92.0	10	13	US-10-050-688-1
8	46	92.0	10	13	US-10-050-688-2
9	32	64.0	10	10	US-09-572-404B-606
10	28	56.0	10	10	US-09-572-404B-3584
11	27	54.0	10	10	US-09-572-404B-3784
12	27	54.0	10	10	US-09-572-404B-3785
13	26	52.0	10	9	US-09-879-957-55
14	25	50.0	10	10	US-09-572-404B-174
15	25	50.0	10	10	US-09-572-404B-2027

16	25	50.0	10	10	US-09-572-404B-2033	Sequence 2033, Ap
17	25	50.0	10	10	US-09-572-404B-2091	Sequence 2091, Ap
18	25	50.0	10	10	US-09-572-404B-2093	Sequence 2093, Ap
19	25	50.0	10	10	US-09-572-404B-2095	Sequence 2095, Ap
20	25	50.0	10	10	US-09-572-270A-136	Sequence 136, Ap
21	25	50.0	10	10	US-09-572-270A-204	Sequence 204, Ap
22	25	50.0	10	10	US-09-572-270A-206	Sequence 206, Ap
23	25	50.0	10	14	US-10-155-333-9	Sequence 9, Appl
24	24	48.0	10	10	US-09-572-404B-4	Sequence 4, Appl
25	24	48.0	10	10	US-09-572-270A-277	Sequence 277, Ap
26	24	48.0	10	10	US-09-572-270A-281	Sequence 281, Ap
27	24	48.0	10	10	US-09-572-270A-283	Sequence 283, Ap
28	24	48.0	10	10	US-09-572-270A-285	Sequence 285, Ap
29	24	48.0	10	10	US-09-572-270A-293	Sequence 293, Ap
30	24	48.0	10	10	US-09-572-270A-295	Sequence 295, Ap
31	24	48.0	10	10	US-09-573-822C-436	Sequence 436, Ap
32	24	48.0	10	13	US-10-008-355-25	Sequence 25, Appl
33	23	46.0	10	9	US-09-879-957-54	Sequence 54, Appl
34	23	46.0	10	10	US-09-572-404B-114	Sequence 114, Ap
35	23	46.0	10	10	US-09-572-404B-176	Sequence 176, Ap
36	23	46.0	10	10	US-09-572-404B-342	Sequence 342, Ap
37	23	46.0	10	10	US-09-572-404B-344	Sequence 344, Ap
38	23	46.0	10	10	US-09-572-404B-1306	Sequence 1306, Ap
39	23	46.0	10	10	US-09-572-404B-2318	Sequence 2318, Ap
40	23	46.0	10	10	US-09-572-404B-2332	Sequence 2332, Ap
41	23	46.0	10	10	US-09-572-404B-2668	Sequence 2668, Ap
42	23	46.0	10	10	US-09-572-404B-2798	Sequence 2798, Ap
43	23	46.0	10	10	US-09-572-404B-3352	Sequence 3352, Ap
44	23	46.0	10	10	US-09-572-404B-3354	Sequence 3354, Ap
45	23	46.0	10	10	US-09-572-404B-3356	Sequence 3356, Ap

ALIGNMENTS

RESULT 1

US-09-909-348-1

; Sequence 1, Application US/09909348

; Patent No. US20020042373A1

; GENERAL INFORMATION:

; APPLICANT: Carney, Darrell H.

; APPLICANT: Crowther, Roger S.

; APPLICANT: Stierberg, Janet

; APPLICANT: Bergmann, John

; TITLE OF INVENTION: Stimulation Of Cartilage Growth With Agonists

; TITLE OF INVENTION: Of The No. US20020042373A1 Proteolytically Activated Thrombin Re

; FILE REFERENCE: 3033.1003-001

; CURRENT APPLICATION NUMBER: US/09/909,348

; PRIOR FILING DATE: 2001-07-19

; PRIOR APPLICATION NUMBER: US 60/219,800

; PRIOR FILING DATE: 2000-07-20

; NUMBER OF SEQ ID NOS: 5

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Peptide fragment of Thrombin

US-09-909-348-1

Query Match 92.0%; Score 46; DB 9; Length 10;

Best Local Similarity 80.0%; Pred. No. 0.37; Indels 0; Gaps 0;

Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CXGDSGGPXY 10

Db 1 CXGDSGGPXY 10

RESULT 2

US-09-909-348-2

; Sequence 2, Application US/09909348

Patent No. US20020042373A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; APPLICANT: Crowther, Roger S.
; APPLICANT: Stienberg, Janet
; APPLICANT: Bergmann, John
; TITLE OF INVENTION: Stimulation Of Cartilage Growth With Agonists
; TITLE OF INVENTION: Of The No. US20020042373A1-Proteolytically Activated Thrombin Re
; FILE REFERENCE: 3033.1003-001
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US/09/909,348
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/219,800
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide fragment of Thrombin
; NAME/KEY: VARIANT
; LOCATION: (1)...(10)
; OTHER INFORMATION: Xaa at position two is Glu or Gln
; OTHER INFORMATION: Xaa at position nine is Phe, Met, Leu, His or Val
US-09-909-348-2

Query Match 92.0%; Score 46; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.37; 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXGDSGGPXV 10
Db 1 CXGDSGGPXV 10

RESULT 3

US-09-909-122-1
; Sequence 1, Application US/09909122
; Patent No. US20020128202A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; APPLICANT: Crowther, Roger S.
; APPLICANT: Simmons, David J.
; APPLICANT: Yang, Jinping
; APPLICANT: Redin, William R.
; TITLE OF INVENTION: Stimulation Of Bone Growth With Thrombin
; TITLE OF INVENTION: Peptide Derivatives
; FILE REFERENCE: 3033.1002-001
; CURRENT APPLICATION NUMBER: US/09/909,122
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/219,300
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide fragment of Thrombin
US-09-909-122-1

Query Match 92.0%; Score 46; DB 9; Length 10;
Best Local Similarity 80.0%; Pred. No. 0.37; 2; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CXGDSGGPXV 10
Db 1 CXGDSGGPXV 10

RESULT 4

US-09-909-122-2
; Sequence 2, Application US/09909122
; Patent No. US20020128202A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; APPLICANT: Crowther, Roger S.
; APPLICANT: Simmons, David J.
; APPLICANT: Yang, Jinping
; APPLICANT: Redin, William R.
; TITLE OF INVENTION: Stimulation Of Bone Growth With Thrombin
; TITLE OF INVENTION: Peptide Derivatives
; FILE REFERENCE: 3033.1002-001
; CURRENT APPLICATION NUMBER: US/09/909,122
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/219,300
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fragment of human prothrombin
US-10-050-692-1

Query Match 92.0%; Score 46; DB 13; Length 10;
Best Local Similarity 80.0%; Pred. No. 0.37; 2; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CXGDSGGPXV 10


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Db 1 CEGDSGGPFV 10
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RESULT 6
US-10-050-692-2
; Sequence 2, Application US/10050692
; Publication No. US20020182205A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; APPLICANT: Crowther, Roger S.
; APPLICANT: Simmons, David J.
; APPLICANT: Yang, Jindong
; APPLICANT: Redin, William R.
; TITLE OF INVENTION: STIMULATION OF BONE GROWTH WITH THROMBIN
; FILE REFERENCE: 3033.1002-004
; CURRENT APPLICATION NUMBER: US/10/050,692
; CURRENT FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: 09/909,122
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/219,300
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human fragment of prothrombin
; NAME/KEY: VARIANT
; LOCATION: (2)...(2)
; OTHER INFORMATION: Xaa = Glu or Gln
; NAME/KEY: VARIANT
; LOCATION: (9)...(9)
; OTHER INFORMATION: Xaa = Phe, Met, Leu, His or Val
US-10-050-692-2
Query Match 92.0%; Score 46; DB 13; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CXGDSGGPFV 10
| | | | | | | |
Db 1 CXGDSGGPFV 10
| | | | | | | |
RESULT 7
US-10-050-688-1
; Sequence 1, Application US/10050688
; Publication No. US20020198154A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; APPLICANT: Crowther, Roger S.
; APPLICANT: Stierberg, Janet
; APPLICANT: Bergmann, John
; TITLE OF INVENTION: STIMULATION OF CARTILAGE GROWTH WITH
; FILE REFERENCE: 3033.1003-004
; CURRENT APPLICATION NUMBER: US/10/050,688
; CURRENT FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: 09/909,348
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/219,800
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide fragment of thrombin
; NAME/KEY: VARIANT
; LOCATION: (2)...(2)
; OTHER INFORMATION: Xaa = Glu or Gln
; NAME/KEY: VARIANT
; LOCATION: (9)...(9)
; OTHER INFORMATION: Xaa = Phe, Met, Leu, His or Val
US-10-050-688-2
Query Match 92.0%; Score 46; DB 13; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CXGDSGGPFV 10
| | | | | | | |
Db 1 CXGDSGGPFV 10
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RESULT 8
US-10-050-688-2
; Sequence 2, Application US/10050688
; Publication No. US20020198154A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; APPLICANT: Crowther, Roger S.
; APPLICANT: Stierberg, Janet
; APPLICANT: Bergmann, John
; TITLE OF INVENTION: STIMULATION OF CARTILAGE GROWTH WITH
; FILE REFERENCE: 3033.1003-004
; CURRENT APPLICATION NUMBER: US/10/050,688
; CURRENT FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: 09/909,348
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/219,800
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide fragment of thrombin
; NAME/KEY: VARIANT
; LOCATION: (2)...(2)
; OTHER INFORMATION: Xaa = Glu or Gln
; NAME/KEY: VARIANT
; LOCATION: (9)...(9)
; OTHER INFORMATION: Xaa = Phe, Met, Leu, His or Val
US-10-050-688-2
Query Match 92.0%; Score 46; DB 13; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CXGDSGGPFV 10
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Db 1 CXGDSGGPFV 10
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RESULT 9
US-09-572-404B-606
; Sequence 606, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide fragment of thrombin
US-10-050-688-1
Query Match 92.0%; Score 46; DB 13; Length 10;
Best Local Similarity 80.0%; Pred. No. 0.37;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CXGDSGGPFV 10
| | | | | | | |
Db 1 CEGDSGGPFV 10
| | | | | | | |
RESULT 8
US-10-050-688-2
; Sequence 2, Application US/10050688
; Publication No. US20020198154A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; APPLICANT: Crowther, Roger S.
; APPLICANT: Stierberg, Janet
; APPLICANT: Bergmann, John
; TITLE OF INVENTION: STIMULATION OF CARTILAGE GROWTH WITH
; FILE REFERENCE: 3033.1003-004
; CURRENT APPLICATION NUMBER: US/10/050,688
; CURRENT FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: 09/909,348
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/219,800
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide fragment of thrombin
; NAME/KEY: VARIANT
; LOCATION: (2)...(2)
; OTHER INFORMATION: Xaa = Glu or Gln
; NAME/KEY: VARIANT
; LOCATION: (9)...(9)
; OTHER INFORMATION: Xaa = Phe, Met, Leu, His or Val
US-10-050-688-2
Query Match 92.0%; Score 46; DB 13; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CXGDSGGPFV 10
| | | | | | | |
Db 1 CXGDSGGPFV 10
| | | | | | | |
RESULT 9
US-09-572-404B-606
; Sequence 606, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
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; SEQ ID NO 606
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
;
; FEATURE:
; OTHER INFORMATION: sequence located in C2 at 674-683 and may interact with Sequence
; OTHER INFORMATION: this patent.
US-09-572-404B-606

Query Match 64.0%; Score 32; DB 10; Length 10;
Best Local Similarity 71.4%; Pred. No. 71;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CKXGSGG 7
| | | | |
Db 2 CKGESGG 8
| | | | |

RESULT 10
US-09-572-404B-3584
; Sequence 3584, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 3584
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
;
; FEATURE:
; OTHER INFORMATION: sequence located in PX1 OR PEX5 at 811-820 and may interact with
; OTHER INFORMATION: Sequence 3583 in this patent.
US-09-572-404B-3584

Query Match 56.0%; Score 28; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GDSGG 7
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Db 6 GDSGG 10
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RESULT 11
US-09-572-404B-3784
; Sequence 3784, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 3784
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
;
; FEATURE:
; OTHER INFORMATION: sequence located in ERK5 OR ERK4 at 543-552 and may interact with
; OTHER INFORMATION: Sequence 3785 in this patent.
US-09-572-404B-3784

Query Match 54.0%; Score 27; DB 10; Length 10;
Best Local Similarity 83.3%; Pred. No. 4.7e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GDSGGP 8
| | | | |
Db 3 GASGGP 8
| | | | |

RESULT 12
US-09-572-404B-3785
; Sequence 3785, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 3785
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
;
; FEATURE:
; OTHER INFORMATION: sequence located in ERK5 OR ERK4 at 543-552 and may interact with
; OTHER INFORMATION: Sequence 3784 in this patent.
US-09-572-404B-3785

Query Match 54.0%; Score 27; DB 10; Length 10;
Best Local Similarity 83.3%; Pred. No. 4.7e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GDSGGP 8
| | | | |
Db 3 GASGGP 8
| | | | |

RESULT 13
US-09-979-957-55
; Sequence 55, Application US/09879957
; Patent No. US20020034755A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; HOFFMAN, No. US20020034755A1h
; KAY, Brian K.
; FOWLKES, Dana M.
; MCCONNELL, Stephen J.
; TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
; DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
; USING SAME
; NUMBER OF SEQUENCES: 227
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/879,957
; FILING DATE: 13-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,915
; FILING DATE: 03-Apr-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-174
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Other
LOCATION: 8
OTHER INFORMATION: Undefined
SEQUENCE DESCRIPTION: SEQ ID NO: 55:
US-09-879-957-55

Query Match 52.0%; Score 26; DB 9; Length 10;
Best Local Similarity 71.4%; Pred. No. 6.8e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CXGDSGG 7
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Db 1 CMGDSL 7

RESULT 14
US-09-572-404B-174
; Sequence 174, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572.404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 174
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: Sequence located in EPHB4 OR HTK at 974-983 and may interact with
; OTHER INFORMATION: Sequence 173 in this patent.
US-09-572-404B-174

Query Match 50.0%; Score 25; DB 10; Length 10;
Best Local Similarity 66.7%; Pred. No. 9.9e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GDSGGP 8
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Db 5 GGTGGP 10

RESULT 15
US-09-572-404B-2027
; Sequence 2027, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572.404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 2027
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:

OTHER INFORMATION: sequence located in CNTFR at 340-349 and may interact with Sequenc
; OTHER INFORMATION: in this patent.
US-09-572-404B-2027

Query Match 50.0%; Score 25; DB 10; Length 10;
Best Local Similarity 66.7%; Pred. No. 9.9e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GDSGGP 8
| | | |
Db 2 GSGGGP 7

Search completed: March 18, 2004, 07:26:10
Job time : 33.5 secs

OTHER INFORMATION: sequence located in EPHB4 OR HTK at 974-983 and may interact with
; OTHER INFORMATION: Sequence 173 in this patent.

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 18, 2004, 07:16:14 ; Search time 26.1905 Seconds
(without alignments)
98.874 Million cell updates/sec

Title: US-09-909-348-2
Perfect score: 50
Sequence: 1 CXGDSGGPXV 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1049977 seqs, 259955339 residues

Total number of hits satisfying chosen parameters: 1049977

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:

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5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/FCUS_PUBCOMB.pep.*
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15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	47	94.0	54	10	US-09-860-739-5
2	47	94.0	237	10	US-09-860-739-1
3	47	94.0	237	14	US-10-128-966-7
4	47	94.0	252	14	US-10-148-671-21
5	47	94.0	261	9	US-09-796-294-10
6	47	94.0	261	9	US-09-822-827-946
7	47	94.0	261	9	US-09-963-896-6
8	47	94.0	261	9	US-09-307-402-1
9	47	94.0	261	9	US-09-895-793-946
10	47	94.0	261	14	US-10-131-241-62
11	47	94.0	261	14	US-10-461-787-10
12	47	94.0	261	15	US-10-298-965-18
13	47	94.0	261	15	US-10-013-697-1558
14	47	94.0	261	15	US-10-341-434-34
15	47	94.0	261	15	US-10-341-434-41

16	47	94.0	261	15	US-10-117-937-78	Sequence 78, Appl
17	47	94.0	261	15	US-10-245-871-358	Sequence 358, Appl
18	47	94.0	261	16	US-10-378-449-2	Sequence 2, Appl
19	47	94.0	262	15	US-10-298-965-14	Sequence 14, Appl
20	47	94.0	282	15	US-10-051-874-97	Sequence 97, Appl
21	47	94.0	296	14	US-10-148-671-17	Sequence 17, Appl
22	47	94.0	322	15	US-10-051-874-96	Sequence 96, Appl
23	47	94.0	366	15	US-10-038-248A-61	Sequence 61, Appl
24	47	94.0	366	15	US-10-074-978A-218	Sequence 218, Appl
25	47	94.0	366	15	US-10-107-782-61	Sequence 61, Appl
26	47	94.0	375	9	US-09-755-100-11	Sequence 11, Appl
27	47	94.0	375	15	US-10-298-965-11	Sequence 11, Appl
28	47	94.0	679	9	US-09-874-198-6	Sequence 6, Appl
29	47	94.0	679	9	US-09-874-238-6	Sequence 2, Appl
30	47	94.0	699	15	US-10-388-322-2	Sequence 2, Appl
31	47	94.0	1019	14	US-10-183-982-4	Sequence 4, Appl
32	47	94.0	1019	14	US-10-183-982-8	Sequence 8, Appl
33	47	94.0	1079	9	US-09-822-827-947	Sequence 947, Appl
34	47	94.0	1079	9	US-09-895-793-947	Sequence 947, Appl
35	47	94.0	1083	14	US-10-183-992-6	Sequence 6, Appl
36	46	92.0	10	9	US-09-909-348-1	Sequence 1, Appl
37	46	92.0	10	9	US-09-909-348-2	Sequence 2, Appl
38	46	92.0	10	9	US-09-909-122-1	Sequence 1, Appl
39	46	92.0	10	9	US-09-909-122-2	Sequence 2, Appl
40	46	92.0	10	13	US-10-050-892-1	Sequence 1, Appl
41	46	92.0	10	13	US-10-050-892-2	Sequence 2, Appl
42	46	92.0	10	13	US-10-050-888-1	Sequence 1, Appl
43	46	92.0	10	13	US-10-050-888-2	Sequence 2, Appl
44	46	92.0	12	9	US-09-879-792-16	Sequence 16, Appl
45	46	92.0	12	9	US-09-904-090-2	Sequence 2, Appl

ALIGNMENTS

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RESULT 1
US-09-860-739-5
; Sequence 5, Application US/09860739
; Publication No. US20030166036A1
; GENERAL INFORMATION:
; APPLICANT: Hybritech Incorporated
; APPLICANT: Mikolajczyk, Stephen
; TITLE OF INVENTION: A Prostate and an Aminopeptidase Associated with Development of B
; TITLE OF INVENTION: Prostatic Hyperplasia (BPH)
; FILE REFERENCE: 2024-451
; CURRENT APPLICATION NUMBER: US/09/860,739
; CURRENT FILING DATE: 2001-05-18
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 5
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-860-739-5
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Query Match 94.0%; Score 47; DB 10; Length 54;
Best Local Similarity 80.0%; Pred. No. 1.2; Mismatches 2; Indels 0; Gaps 0;
Matches 8; Conservative 0

Qy 1 CXGDSGGPXV 10
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Db 2 CSXGDSGGPLV 11

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RESULT 2
US-09-860-739-1
; Sequence 1, Application US/09860739
; Publication No. US20030166036A1
; GENERAL INFORMATION:
; APPLICANT: Hybritech Incorporated
; APPLICANT: Mikolajczyk, Stephen
; APPLICANT: Rittenhouse, Harry
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; TITLE OF INVENTION: A Protease and an Aminopeptidase Associated with Development of B
; TITLE OF INVENTION: Prostatic Hyperplasia (BPH)
; FILE REFERENCE: 2024-451
; CURRENT APPLICATION NUMBER: US/09/860,739
; CURRENT FILING DATE: 2001-05-18
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-860-739-1
Query Match          94.0%; Score 47; DB 10; Length 237;
Best Local Similarity 80.0%; Pred. No. 4.6;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CXGDSGGPXV 10
Db 185 CSGDSGGPLV 194

RESULT 3
US-10-128-966-7
; Sequence 7, Application US/10128966
; Publication No. US20030113743A1
; GENERAL INFORMATION:
; APPLICANT: Slawin, K.M.
; APPLICANT: Tindall, D.J.
; APPLICANT: Young, C.Y.F.
; APPLICANT: Saedi, M.S.
; APPLICANT: Kumar, A.
; APPLICANT: Rittenhouse, H.G.
; APPLICANT: Wolfert, R.L.
; TITLE OF INVENTION: Method for detection of micrometastatic
; FILE REFERENCE: 675 001US1
; CURRENT APPLICATION NUMBER: US/10/128,966
; CURRENT FILING DATE: 2002-04-22
; PRIOR APPLICATION NUMBER: US/08/843,076D
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: US 08/759,354
; PRIOR FILING DATE: 1996-11-14
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-128-966-7
Query Match          94.0%; Score 47; DB 14; Length 237;
Best Local Similarity 80.0%; Pred. No. 4.6;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CXGDSGGPXV 10
Db 185 CSGDSGGPLV 194

RESULT 4
US-10-148-671-21
; Sequence 21, Application US/10148671
; Publication No. US20030186419A1
; GENERAL INFORMATION:
; APPLICANT: Jensenius, Jens Christian
; APPLICANT: Thiel, Steffen
; TITLE OF INVENTION: NASP-3, A complement-fixing enzyme, and uses for it
; FILE REFERENCE: 10/148,671
; CURRENT APPLICATION NUMBER: US/10/148,671
; CURRENT FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: PCT/DK00/00659
; PRIOR FILING DATE: 2000-11-30

; TITLE OF INVENTION: A Protease and an Aminopeptidase Associated with Development of B
; TITLE OF INVENTION: Prostatic Hyperplasia (BPH)
; FILE REFERENCE: 2024-451
; CURRENT APPLICATION NUMBER: US/09/860,739
; CURRENT FILING DATE: 2001-05-18
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Homo sapiens (fig. 10, hUMASP-1)
US-10-148-671-21
Query Match          94.0%; Score 47; DB 14; Length 252;
Best Local Similarity 80.0%; Pred. No. 4.9;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CXGDSGGPXV 10
Db 195 CAGDSGGPMV 204

RESULT 5
US-09-796-294-10
; Sequence 10, Application US/09796294
; Patent No. US20020037581A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Underwood, Lowell J.
; TITLE OF INVENTION: Extracellular Serine Protease
; FILE REFERENCE: D6020CIP3
; CURRENT APPLICATION NUMBER: US/09/796,294
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 09/618,259
; PRIOR FILING DATE: 2000-07-18
; NUMBER OF SEQ ID NOS: 72
; SEQ ID NO 10
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of Prostate Specific Antigen
; OTHER INFORMATION: (hPSA); accession no. P07288
US-09-796-294-10
Query Match          94.0%; Score 47; DB 9; Length 261;
Best Local Similarity 80.0%; Pred. No. 5.1;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CXGDSGGPXV 10
Db 209 CSGDSGGPLV 218

RESULT 6
US-09-822-827-946
; Sequence 946, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 946
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-822-827-946
Query Match          94.0%; Score 47; DB 9; Length 261;
Best Local Similarity 80.0%; Pred. No. 5.1;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CXGDSGGPXV 10
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Db 209 CSGDSGGPLV 218
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RESULT 7
US-09-963-896-6
; Sequence 6, Application US/09963896
; Patent No. US20020102585A1
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; Guegler, Karl J.
; Corley, Neil C.
; TITLE OF INVENTION: PROSTATE GROWTH-ASSOCIATED MEMBRANE PROTEINS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/963,896
; FILING DATE: 26-Sep-2001
; CLASSIFICATION: <Unknown>
; APPLICATION DATA:
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: CERRONE, MICHAEL C.
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0527 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 261 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 130989
; SEQUENCE DESCRIPTION: SEQ ID NO: 6 :
US-09-963-896-6
Query Match 94.0%; Score 47; DB 9; Length 261;
Best Local Similarity 80.0%; Pred. No. 5.1;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 CXGDSGGPXV 10
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Db 209 CSGDSGGPLV 218
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RESULT 8
US-09-907-402-1
; Sequence 1, Application US/09907402
; Patent No. US20020137668A1
; GENERAL INFORMATION:
; APPLICANT: Holaday, John W.
; APPLICANT: Fortier, Anne H.
; TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Proliferation
; FILE REFERENCE: 05213-0343 43170-261379
; CURRENT APPLICATION NUMBER: US/09/907,402
; CURRENT FILING DATE: 2001-07-17

; PRIOR APPLICATION NUMBER: US 60/086,586
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: US 09/316,802
; PRIOR FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: US 09/413,049
; PRIOR FILING DATE: 1999-10-06
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-907-402-1
Query Match 94.0%; Score 47; DB 9; Length 261;
Best Local Similarity 80.0%; Pred. No. 5.1;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 CXGDSGGPXV 10
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Db 209 CSGDSGGPLV 218
| | | | |
RESULT 9
US-09-895-793-946
; Sequence 946, Application US/09895793
; Publication No. US20020192763A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darriek
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C2
; CURRENT APPLICATION NUMBER: US/09/895,793
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows version 3.0
; SEQ ID NO 946
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-895-793-946
Query Match 94.0%; Score 47; DB 9; Length 261;
Best Local Similarity 80.0%; Pred. No. 5.1;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 CXGDSGGPXV 10
| | | | |
Db 209 CSGDSGGPLV 218
| | | | |
RESULT 10

US-10-131-241-62
; Sequence 62, Application US/10131241
; Publication No. US20030012792A1
; GENERAL INFORMATION:
; APPLICANT: Holaday, John W.
; TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Proliferation
; TITLE OF INVENTION: and Regulating Angiogenesis Using Cancer Markers
; FILE REFERENCE: 05213-0344 43170-271565
; CURRENT APPLICATION NUMBER: US/10/131,241
; CURRENT FILING DATE: 2002-07-22
; PRIOR FILING DATE: 1999-10-06
; PRIOR FILING DATE: 1999-05-21
; PRIOR FILING DATE: 1999-05-21
; PRIOR FILING DATE: 1998-05-22
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 62
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-131-241-62

Query Match 94.0%; Score 47; DB 14; Length 261;
Best Local Similarity 80.0%; Pred. No. 5.1;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CXGDSGGPXXV 10
DB 209 CSGDSGGPLV 218

RESULT 11
US-10-461-787-10
; Sequence 10, Application US/10461787
; Publication No. US20030199010A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: No. US20030199010A1 Extracellular Serine Protease
; FILE REFERENCE: D6020CIP2
; CURRENT APPLICATION NUMBER: US/10/461,787
; PRIOR FILING DATE: 2003-06-13
; PRIOR FILING DATE: 2000-07-18
; PRIOR FILING DATE: 1998-08-21
; NUMBER OF SEQ ID NOS: 72
; SEQ ID NO 10
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: Amino acid sequence of Prostate Specific Antigen
; OTHER INFORMATION: (hpsa); accession no. P07288
US-10-461-787-10

Query Match 94.0%; Score 47; DB 14; Length 261;
Best Local Similarity 80.0%; Pred. No. 5.1;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CXGDSGGPXXV 10
DB 209 CSGDSGGPLV 218

RESULT 12
US-10-298-965-18
; Sequence 18, Application US/10298965
; Publication No. US20030207808A1
; GENERAL INFORMATION:

APPLICANT: SAVITZKY, Kinmeret et al.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID AND AMINO ACID SEQUENCES
; FILE REFERENCE: 2786-0231P
; CURRENT APPLICATION NUMBER: US/10/298,965
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: IL 128587
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: IL 129439
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: IL 131363
; PRIOR FILING DATE: 1999-08-11
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 18
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-298-965-18

Query Match 94.0%; Score 47; DB 15; Length 261;
Best Local Similarity 80.0%; Pred. No. 5.1;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CXGDSGGPXXV 10
DB 209 CSGDSGGPLV 218

RESULT 13
US-10-012-697-1558
; Sequence 1558, Application US/10012697
; Publication No. US20030215803A1
; GENERAL INFORMATION:
; APPLICANT: Escobedo, Jaime
; APPLICANT: Garcia, Pablo Dominguez
; APPLICANT: Kassam, Altaf
; APPLICANT: Lamson, George
; APPLICANT: Scott, Beth
; APPLICANT: Drmanac, Radoje
; APPLICANT: Crkvenjakov, Radomir
; APPLICANT: Dickson, Mark
; APPLICANT: Drmanac, Snezana
; APPLICANT: Labat, Ivan
; APPLICANT: Leshkowitz, Dena
; APPLICANT: Kita, David
; APPLICANT: Garcia, Veronica
; APPLICANT: Jones, Lee William
; APPLICANT: Stache-Crain, Birgit
; TITLE OF INVENTION: HUMAN GENES AND GENE EXPRESSION PRODUCTS
; TITLE OF INVENTION: ISOLATED FROM HUMAN PROSTATE
; FILE REFERENCE: 2300-16252
; CURRENT APPLICATION NUMBER: US/10/012,697
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: 60/254,648
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 60/275,668
; PRIOR FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 1568
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1558
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-012-697-1558

Query Match 94.0%; Score 47; DB 15; Length 261;
Best Local Similarity 80.0%; Pred. No. 5.1;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CXGDSGGPXXV 10
DB 209 CSGDSGGPLV 218

RESULT 14
 US-10-341-434-34
 ; Sequence 34, Application US/10341434
 ; Publication No. US20030215835A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Origene Technologies
 ; TITLE OF INVENTION: Differentially Regulated Prostate Cancer Genes
 ; FILE REFERENCE: 9U 204 205 R1
 ; CURRENT APPLICATION NUMBER: US/10/341,434
 ; CURRENT FILING DATE: 2003-07-18
 ; PRIOR APPLICATION NUMBER: US 60/348,164
 ; PRIOR FILING DATE: 2002-01-15
 ; PRIOR APPLICATION NUMBER: US 60/348,119
 ; PRIOR FILING DATE: 2002-01-15
 ; NUMBER OF SEQ ID NOS: 238
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 34
 ; LENGTH: 261
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-341-434-34

Query Match 94.0%; Score 47; DB 15; Length 261;
 Best Local Similarity 80.0%; Pred. No. 5.1;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CXGDSGGPXV 10
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 Db 209 CSGDSGGPLV 218

RESULT 15
 US-10-341-434-41
 ; Sequence 41, Application US/10341434
 ; Publication No. US20030215835A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Origene Technologies
 ; TITLE OF INVENTION: Differentially Regulated Prostate Cancer Genes
 ; FILE REFERENCE: 9U 204 205 R1
 ; CURRENT APPLICATION NUMBER: US/10/341,434
 ; CURRENT FILING DATE: 2003-07-18
 ; PRIOR APPLICATION NUMBER: US 60/348,164
 ; PRIOR FILING DATE: 2002-01-15
 ; PRIOR APPLICATION NUMBER: US 60/348,119
 ; PRIOR FILING DATE: 2002-01-15
 ; NUMBER OF SEQ ID NOS: 238
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 41
 ; LENGTH: 261
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-341-434-41

Query Match 94.0%; Score 47; DB 15; Length 261;
 Best Local Similarity 80.0%; Pred. No. 5.1;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CXGDSGGPXV 10
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 Db 209 CSGDSGGPLV 218

Search completed: March 18, 2004, 07:24:51
 Job time : 26.1905 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 18, 2004, 07:17:54 ; Search time 39 Seconds
(without alignments)
26.560 Million cell updates/sec

Title: US-09-909-348-3

Perfect score: 21

Sequence: 1 RGDA 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1049977 seqs, 25895339 residues

Total number of hits satisfying chosen parameters: 5333

Minimum DB seq length: 4

Maximum DB seq length: 4

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:

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3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
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5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
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18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	21	100.0	4	9 US-09-904-090-1	Sequence 1, Appli
3	21	100.0	4	9 US-09-909-122-3	Sequence 3, Appli
4	21	100.0	4	10 US-09-911-569-23	Sequence 23, Appli
5	21	100.0	4	13 US-10-050-692-3	Sequence 3, Appli
6	21	100.0	4	13 US-10-050-611-1	Sequence 1, Appli
7	21	100.0	4	13 US-10-050-688-3	Sequence 3, Appli
8	21	100.0	4	14 US-10-200-879-23	Sequence 23, Appli
9	18	85.7	4	9 US-09-823-444-6	Sequence 6, Appli
10	18	85.7	4	9 US-09-010-714-9	Sequence 9, Appli
11	18	85.7	4	9 US-09-925-715-21	Sequence 21, Appli
12	18	85.7	4	9 US-09-935-168-1	Sequence 1, Appli
13	18	85.7	4	9 US-09-942-117-5	Sequence 5, Appli
14	18	85.7	4	10 US-09-911-569-22	Sequence 22, Appli
15	18	85.7	4	11 US-09-991-588B-23	Sequence 23, Appli

16	18	85.7	4	12	US-10-169-085-23	Sequence 23, Appli
17	18	85.7	4	14	US-10-046-801-4	Sequence 4, Appli
18	18	85.7	4	14	US-10-215-435-5	Sequence 5, Appli
19	18	85.7	4	14	US-10-200-879-22	Sequence 22, Appli
20	18	85.7	4	14	US-10-021-660-130	Sequence 130, Appli
21	18	85.7	4	14	US-10-299-043-1	Sequence 1, Appli
22	18	85.7	4	14	US-10-300-694A-96	Sequence 96, Appli
23	18	85.7	4	14	US-10-405-339-60	Sequence 60, Appli
24	18	85.7	4	14	US-10-279-733-17	Sequence 17, Appli
25	18	85.7	4	15	US-10-237-429-39	Sequence 39, Appli
26	18	85.7	4	15	US-10-441-965-11	Sequence 11, Appli
27	18	85.7	4	16	US-10-208-894A-2	Sequence 2, Appli
28	17	81.0	4	9	US-09-892-071-4	Sequence 4, Appli
29	17	81.0	4	9	US-09-051-603-173	Sequence 173, Appli
30	17	81.0	4	9	US-09-051-603-175	Sequence 175, Appli
31	17	81.0	4	9	US-09-961-834-4	Sequence 4, Appli
32	17	81.0	4	9	US-09-961-834-5	Sequence 5, Appli
33	17	81.0	4	9	US-09-765-614B-1	Sequence 1, Appli
34	17	81.0	4	9	US-09-925-715-4	Sequence 4, Appli
35	17	81.0	4	9	US-09-972-772-32	Sequence 32, Appli
36	17	81.0	4	10	US-09-911-569-16	Sequence 16, Appli
37	17	81.0	4	10	US-09-911-569-18	Sequence 18, Appli
38	17	81.0	4	10	US-09-911-569-19	Sequence 19, Appli
39	17	81.0	4	10	US-09-911-569-20	Sequence 20, Appli
40	17	81.0	4	10	US-09-911-569-21	Sequence 21, Appli
41	17	81.0	4	11	US-09-991-588B-1	Sequence 1, Appli
42	17	81.0	4	11	US-09-991-588B-2	Sequence 2, Appli
43	17	81.0	4	13	US-10-001-945-32	Sequence 32, Appli
44	17	81.0	4	14	US-10-215-435-7	Sequence 7, Appli
45	17	81.0	4	14	US-10-215-435-10	Sequence 10, Appli

ALIGNMENTS

RESULT 1
US-09-909-348-3
; Sequence 3, Application US/09909348
; Patent No. US20020042373A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; APPLICANT: Crowther, Roger S.
; APPLICANT: Stierberg, Janet
; APPLICANT: Bergmann, John
; TITLE OF INVENTION: Stimulation Of Cartilage Growth With Agonists
; TITLE OF INVENTION: Of The No. US20020042373A1-Proteolytically Activated Thrombin Re
; FILE REFERENCE: 3033.1003-001
; CURRENT APPLICATION NUMBER: US/09/909,348
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/219,800
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide fragment of Thrombin
US-09-909-348-3

Query Match 100.0%; Score 21; DB 9; Length 4;
Best Local Similarity 100.0%; Pred. No. 9.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGDA 4
Db 1 RGDA 4

RESULT 2

US-09-904-090-1
; Sequence 1, Application US/09904090

Patent No. US20020061852A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell
; TITLE OF INVENTION: METHODS OF THERAPY WITH THROMBIN DERIVED
; TITLE OF INVENTION: PEPTIDE-ENHANCED TRANSECTIONS
; NUMBER OF SEQUENCES: 120
; FILE REFERENCE: 3033.1000-001
; CURRENT APPLICATION NUMBER: US/09/904,090
; CURRENT FILING DATE: 2001-07-12
; PRIOR FILING DATE: 2000-07-12
; PRIOR FILING DATE: 2000-07-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide, fragment of thrombin
US-09-904-090-1

Query Match 100.0%; Score 21; DB 9; Length 4;
Best Local Similarity 100.0%; Pred. No. 9.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGDA 4
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Db 1 RGDA 4

RESULT 3
US-09-909-122-3
; Sequence 3, Application US/09909122
; Patent No. US20020128202A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; APPLICANT: Crowther, Roger S.
; APPLICANT: Simmons, David J.
; APPLICANT: Yang, Jinping
; APPLICANT: Redin, William R.
; TITLE OF INVENTION: Stimulation Of Bone Growth With Thrombin
; TITLE OF INVENTION: Peptide Derivatives
; FILE REFERENCE: 3033.1002-001
; CURRENT APPLICATION NUMBER: US/09/909,122
; CURRENT FILING DATE: 2001-07-19
; PRIOR FILING DATE: 2000-07-19
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide fragment of Thrombin
US-09-909-122-3

Query Match 100.0%; Score 21; DB 9; Length 4;
Best Local Similarity 100.0%; Pred. No. 9.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGDA 4
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Db 1 RGDA 4

RESULT 4
US-09-911-569-23
; Sequence 23, Application US/09911569
; Publication No. US20030069173A1
; GENERAL INFORMATION:
; APPLICANT: HAWLEY-NELSON, PAMELA
; APPLICANT: LAN, JIANQING
; APPLICANT: SHIH, FOUEN

JESSE, JOEL A.
SCHIFFERLI, KEVIN P.
GESEYERU, GULILAT
; TITLE OF INVENTION: PEPTIDE-ENHANCED TRANSECTIONS
; NUMBER OF SEQUENCES: 120
; CORRESPONDENCE ADDRESS:
ADDRESSEE: GREENLEE, WINNER & SULLIVAN
STREET: 5370 MANHATTAN CIRCLE, SUITE 201
CITY: BOULDER
STATE: CO
COUNTRY: US
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/911,569
FILING DATE: 23-Jul-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/039,780
FILING DATE: 16-MAR-1998
ATTORNEY/AGENT INFORMATION:
NAME: SULLIVAN, SALLY A.
REGISTRATION NUMBER: 32,064
REFERENCE/DOCKET NUMBER: 32-95D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303)499-8080
TELEFAX: (303)499-8089
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHEICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-911-569-23

Query Match 100.0%; Score 21; DB 10; Length 4;
Best Local Similarity 100.0%; Pred. No. 9.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGDA 4
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Db 1 RGDA 4

RESULT 5
US-10-050-692-3
; Sequence 3, Application US/10050692
; Publication No. US20020182205A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; APPLICANT: Crowther, Roger S.
; APPLICANT: Simmons, David J.
; APPLICANT: Yang, Jinping
; APPLICANT: Redin, William R.
; TITLE OF INVENTION: STIMULATION OF BONE GROWTH WITH THROMBIN
; TITLE OF INVENTION: PEPTIDE DERIVATIVES
; FILE REFERENCE: 3033.1002-004
; CURRENT APPLICATION NUMBER: US/10/050,692
; CURRENT FILING DATE: 2002-01-16
; PRIOR FILING DATE: 2001-07-19
; PRIOR FILING DATE: 2001-07-19
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 4.0

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; SEQ ID NO 3
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fragment of human prothrombin
US-10-050-692-3

Query Match          100.0%; Score 21; DB 13; Length 4;
Best Local Similarity 100.0%; Pred. No. 9.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGDA 4
Db 1 RGDA 4

RESULT 6
US-10-050-611-1
; Sequence 1, Application US/10050611
; Publication No. US20020187933A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; TITLE OF INVENTION: METHODS OF THERAPY WITH THROMBIN DERIVED
; TITLE OF INVENTION: PEPTIDES
; FILE REFERENCE: 3033.1000-008
; CURRENT APPLICATION NUMBER: US/10/050,611
; CURRENT FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: 09/904,090
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 60/217,583
; PRIOR FILING DATE: 2000-07-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human fragment of thrombin
US-10-050-611-1

Query Match          100.0%; Score 21; DB 13; Length 4;
Best Local Similarity 100.0%; Pred. No. 9.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGDA 4
Db 1 RGDA 4

RESULT 7
US-10-050-688-3
; Sequence 3, Application US/10050688
; Publication No. US20020198154A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; APPLICANT: Crowther, Roger S.
; APPLICANT: Stierberg, Janet
; APPLICANT: Bergmann, John
; TITLE OF INVENTION: STIMULATION OF CARTILAGE GROWTH WITH
; TITLE OF INVENTION: AGONISTS OF THE NON-PROTEOLYTICALLY ACTIVATED THROMBIN
; TITLE OF INVENTION: RECEPTOR
; FILE REFERENCE: 3033.1003-004
; CURRENT APPLICATION NUMBER: US/10/050,688
; CURRENT FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: 09/909,348
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/219,800
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
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; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide fragment of thrombin
US-10-050-688-3

Query Match          100.0%; Score 21; DB 13; Length 4;
Best Local Similarity 100.0%; Pred. No. 9.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGDA 4
Db 1 RGDA 4

RESULT 8
US-10-200-879-23
; Sequence 23, Application US/10200879
; Publication No. US20030144230A1
; GENERAL INFORMATION:
; APPLICANT: HAWLEY-NELSON, PAMELA
; APPLICANT: LAN, JIANQING
; APPLICANT: SHIH, POUEH
; APPLICANT: JESSE, JOEL A.
; APPLICANT: SCHIFFERLI, KEVIN P.
; APPLICANT: GEBEYEHU, GULILAT
; TITLE OF INVENTION: PEPTIDE-ENHANCED TRANSECTIONS
; NUMBER OF SEQUENCES: 120
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GREENLEE, WINNER & SULLIVAN
; STREET: 5370 MANHATTAN CIRCLE, SUITE 201
; CITY: BOULDER
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/200,879
; FILING DATE: 23-Jul-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/911,569
; FILING DATE: 23-JUL-2001
; APPLICATION NUMBER: US 09/039,780
; FILING DATE: 16-MAR-1998
; APPLICATION NUMBER: US 08/818,200
; FILING DATE: 14-MAR-1997
; APPLICATION NUMBER: US 08/658,130
; FILING DATE: 04-JUN-1996
; APPLICATION NUMBER: US 08/477,354
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: SULLIVAN, SALLY A.
; REGISTRATION NUMBER: 32,064
; REFERENCE/DOCKET NUMBER: 32-95E
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303)499-8080
; TELEFAX: (303)499-8089
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
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US-10-200-879-23

Query Match 100.0%; Score 21; DB 14; Length 4;
Best Local Similarity 100.0%; Pred. No. 9.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGDA 4
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Db 1 RGDA 4

RESULT 9

US-09-823-444-6
; Sequence 6, Application US/09823444
; Patent No. US2002009753A1
; GENERAL INFORMATION:
; APPLICANT: Bednar, Bohumil
; APPLICANT: Bollag, Daniel M.
; APPLICANT: Gould, Robert J.
; APPLICANT: Merck & Co., Inc.
; TITLE OF INVENTION: ANTICOAGULANT TEST
; FILE REFERENCE: 19910
; CURRENT APPLICATION NUMBER: US/09/823,444
; CURRENT FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: This sequence is a synthetically prepared peptide.

US-09-823-444-6

Query Match 85.7%; Score 18; DB 9; Length 4;
Best Local Similarity 75.0%; Pred. No. 9.5e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGDA 4
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Db 1 RGDS 4

RESULT 10

US-09-010-714-9
; Sequence 9, Application US/09010714
; Patent No. US20020012942A1
; GENERAL INFORMATION:
; APPLICANT: McCarthy, James B.
; APPLICANT: Furcht, Leo T.
; APPLICANT: Iida, Joji
; TITLE OF INVENTION: POLYPEPTIDES WITH ALPHA 4 INTEGRIN SUBUNIT RELATED
; FILE REFERENCE: 600.332US01
; CURRENT APPLICATION NUMBER: US/09/010,714
; CURRENT FILING DATE: 1998-01-22
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-010-714-9

Query Match 85.7%; Score 18; DB 9; Length 4;
Best Local Similarity 75.0%; Pred. No. 9.5e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGDA 4
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Db 1 RGDS 4

RESULT 11

US-09-925-715-21
; Sequence 21, Application US/09925715
; Patent No. US20020102217A1
; GENERAL INFORMATION:
; APPLICANT: Nycomed Imaging AS
; TITLE OF INVENTION: Improvements in or relating to diagnostic/therapeutic
; FILE REFERENCE: REF/Kiavness/206
; CURRENT APPLICATION NUMBER: US/09/925,715
; CURRENT FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic RGDS
; OTHER INFORMATION: sequence

US-09-925-715-21

Query Match 85.7%; Score 18; DB 9; Length 4;
Best Local Similarity 75.0%; Pred. No. 9.5e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGDA 4
|||
Db 1 RGDS 4

RESULT 12

US-09-935-168-1
; Sequence 1, Application US/09935168
; Patent No. US20020106793A1
; GENERAL INFORMATION:
; APPLICANT: West, Jennifer L.
; APPLICANT: Mann, Brenda K.
; TITLE OF INVENTION: Tissue Engineering Scaffolds Promoting Matrix Protein Production
; FILE REFERENCE: RICE 103
; CURRENT APPLICATION NUMBER: US/09/935,168
; CURRENT FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: cell adhesion ligand

US-09-935-168-1

Query Match 85.7%; Score 18; DB 9; Length 4;
Best Local Similarity 75.0%; Pred. No. 9.5e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGDA 4
|||
Db 1 RGDS 4

RESULT 13

US-09-942-117-5
; Sequence 5, Application US/09942117
; Publication No. US20020197700A1
; GENERAL INFORMATION:
; APPLICANT: MENRAD, ANDREAS
; APPLICANT: REDLITZ, ALEXANDER
; APPLICANT: KOPPLITZ, MARCUS
; APPLICANT: EGNER, URSULA
; APPLICANT: BAHR, INKE
; TITLE OF INVENTION: RECEPTOR OF THE EDB-FIBRONECTIN DOMAINS
; FILE REFERENCE: SCH-1832

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; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-911-569-22

Query Match      85.7%; Score 18; DB 10; Length 4;
Best Local Similarity 75.0%; Pred. NO. 9.5e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 RGDA 4
        |||;
Db      1 RGDS 4

RESULT 15
US-09-991-588B-23
; Sequence 23, Application US/09991588B
; Publication No. US20030219429A1
; GENERAL INFORMATION:
; APPLICANT: Budny, John A.
; TITLE OF INVENTION: Compositionand Method for Bone Regeneration
; FILE REFERENCE: 1008-120.US
; CURRENT APPLICATION NUMBER: US/09/991,588B
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 09/122,348
; PRIOR FILING DATE: 1998-07-24
; NUMBER OF SEQ ID NOS: 23
; SEQ ID NO 23
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Purchased commercially or sequence is synthesized
US-09-991-588B-23

Query Match      85.7%; Score 18; DB 11; Length 4;
Best Local Similarity 75.0%; Pred. NO. 9.5e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 RGDA 4
        |||;
Db      1 RGDS 4

Search completed: March 18, 2004, 07:27:02
Job time : 40 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 18, 2004, 07:16:14 ; Search time 10.4762 Seconds
(without alignments)
98.874 Million cell updates/sec

Title: US-09-909-348-3
Perfect score: 21
Sequence: 1 RGDA 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1049977 seqs, 258955339 residues

Total number of hits satisfying chosen parameters: 1049977

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
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- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/1/pubpaa/US09D_PUBCOMB.pep:*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
- 17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep:*
- 18: /cgn2_6/ptodata/1/pubpaa/US10F_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	4	9	US-09-909-348-3
2	21	100.0	4	9	US-09-904-090-1
3	21	100.0	4	9	US-09-909-122-3
4	21	100.0	4	10	US-09-911-569-23
5	21	100.0	4	13	US-10-050-692-3
6	21	100.0	4	13	US-10-050-611-1
7	21	100.0	4	13	US-10-050-688-3
8	21	100.0	4	14	US-10-200-879-23
9	21	100.0	7	9	US-09-989-789-289
10	21	100.0	7	9	US-09-989-789-670
11	21	100.0	7	9	US-09-989-789-671
12	21	100.0	7	9	US-09-989-789-672
13	21	100.0	7	9	US-09-989-789-673
14	21	100.0	7	9	US-09-989-789-674
15	21	100.0	7	9	US-09-989-789-675

16	21	100.0	7	9	US-09-989-789-696
17	21	100.0	7	9	US-09-989-789-966
18	21	100.0	7	9	US-09-989-789-971
19	21	100.0	7	9	US-09-989-789-1047
20	21	100.0	7	9	US-09-989-789-1048
21	21	100.0	7	9	US-09-989-789-1048
22	21	100.0	7	9	US-09-989-789-1915
23	21	100.0	7	9	US-09-989-789-1924
24	21	100.0	7	9	US-09-989-789-1925
25	21	100.0	7	9	US-09-989-789-1927
26	21	100.0	7	9	US-09-989-789-1928
27	21	100.0	7	9	US-09-989-789-1961
28	21	100.0	7	9	US-09-989-789-1989
29	21	100.0	7	9	US-09-989-789-1990
30	21	100.0	7	9	US-09-989-789-1996
31	21	100.0	7	9	US-09-989-789-1997
32	21	100.0	7	9	US-09-989-789-2005
33	21	100.0	7	9	US-09-989-789-2007
34	21	100.0	7	9	US-09-989-789-2007
35	21	100.0	7	9	US-09-989-789-2007
36	21	100.0	7	9	US-09-989-789-2007
37	21	100.0	7	9	US-09-989-789-2007
38	21	100.0	7	9	US-09-989-789-2007
39	21	100.0	7	9	US-09-989-789-2007
40	21	100.0	7	9	US-09-989-789-2007
41	21	100.0	7	9	US-09-989-789-2007
42	21	100.0	7	9	US-09-989-789-2007
43	21	100.0	7	9	US-09-989-789-2007
44	21	100.0	7	9	US-09-989-789-2007
45	21	100.0	7	9	US-09-989-789-2007

ALIGNMENTS

RESULT 1

US-09-909-348-3
; Sequence 3, Application US/09909348
; Patent No. US20020042373A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; APPLICANT: Crowther, Roger S.
; APPLICANT: Stierberg, Janet
; APPLICANT: Bergmann, John
; TITLE OF INVENTION: Stimulation Of Cartilage Growth With Agonists
; FILE REFERENCE: 3033.1003-001
; CURRENT FILING DATE: 2001-07-19
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide fragment of Thrombin
US-09-909-348-3

Query Match 100.0%; Score 21; DB 9; Length 4;
Best Local Similarity 100.0%; Pred. No. 9.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGDA 4
Db 1 RGDA 4

RESULT 2

US-09-904-090-1
; Sequence 1, Application US/09904090

Patent No. US20020061852A1
GENERAL INFORMATION:
APPLICANT: Carney, Darrell H.
TITLE OF INVENTION: METHODS OF THERAPY WITH THROMBIN DERIVED
PEPTIDES
FILE REFERENCE: 3033.1000-001
CURRENT APPLICATION NUMBER: US/09/904,090
CURRENT FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: US 60/217,583
PRIOR FILING DATE: 2000-07-12
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 4
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Polypeptide, fragment of thrombin
US-09-904-090-1

Query Match 100.0%; Score 21; DB 9; Length 4;
Best Local Similarity 100.0%; Pred. No. 9.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGDA 4
Db 1 RGDA 4

RESULT 3
US-09-909-122-3
Sequence 3, Application US/09909122
Patent No. US20020128202A1
GENERAL INFORMATION:
APPLICANT: Carney, Darrell H.
APPLICANT: Crowther, Roger S.
APPLICANT: Simmons, David J.
APPLICANT: Yang, Jinping
APPLICANT: Redin, William R.
TITLE OF INVENTION: Stimulation Of Bone Growth With Thrombin
Peptide Derivatives
FILE REFERENCE: 3033.1002-001
CURRENT APPLICATION NUMBER: US/09/909,122
CURRENT FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: US 60/219,300
PRIOR FILING DATE: 2000-07-19
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 4
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Peptide fragment of Thrombin
US-09-909-122-3

Query Match 100.0%; Score 21; DB 9; Length 4;
Best Local Similarity 100.0%; Pred. No. 9.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGDA 4
Db 1 RGDA 4

RESULT 4
US-09-911-569-23
Sequence 23, Application US/09911569
Publication No. US20030069173A1
GENERAL INFORMATION:
APPLICANT: HAWLEY-NELSON, PAMELA
LAN, JIANQING
SHIH, POJEN

JESSE, JOEL A.
SCHIPPERLI, KEVIN P.
GBEXEHU, GUILIAT
TITLE OF INVENTION: PEPTIDE-ENHANCED TRANSECTIONS
NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
ADDRESSEE: GREENLEE, WINNER & SULLIVAN
STREET: 5370 MANHATTAN CIRCLE, SUITE 201
CITY: BOULDER
STATE: CO
COUNTRY: US
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/911,569
Filing DATE: 23-Jul-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/039,780
Filing DATE: 16-MAR-1998
ATTORNEY/AGENT INFORMATION:
NAME: SULLIVAN, SALLY A.
REGISTRATION NUMBER: 32,064
REFERENCE/DOCKET NUMBER: 32-95D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303)499-8080
TELEFAX: (303)499-8089
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-911-569-23

Query Match 100.0%; Score 21; DB 10; Length 4;
Best Local Similarity 100.0%; Pred. No. 9.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGDA 4
Db 1 RGDA 4

RESULT 5
US-10-050-692-3
Sequence 3, Application US/10050692
Publication No. US20020182205A1
GENERAL INFORMATION:
APPLICANT: Carney, Darrell H.
APPLICANT: Crowther, Roger S.
APPLICANT: Simmons, David J.
APPLICANT: Yang, Jinping
APPLICANT: Redin, William R.
TITLE OF INVENTION: STIMULATION OF BONE GROWTH WITH THROMBIN
PEPTIDE DERIVATIVES
FILE REFERENCE: 3033.1002-004
CURRENT APPLICATION NUMBER: US/10/050,692
CURRENT FILING DATE: 2002-01-16
PRIOR APPLICATION NUMBER: 09/909,122
PRIOR FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: 60/219,300
PRIOR FILING DATE: 2000-07-19
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSeq for Windows Version 4.0

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; SEQ ID NO 3
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fragment of human prothrombin
US-10-050-692-3

Query Match      100.0%; Score 21; DB 13; Length 4;
Best Local Similarity 100.0%; Pred. No. 9.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RGDA 4
        ||||
Db      1 RGDA 4

RESULT 6
US-10-050-611-1
; Sequence 1, Application US/10050611
; Publication No. US20020187933A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; TITLE OF INVENTION: METHODS OF THERAPY WITH THROMBIN DERIVED
; TITLE OF INVENTION: PEPTIDES
; FILE REFERENCE: 3033.1000-008
; CURRENT APPLICATION NUMBER: US/10/050,611
; CURRENT FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: 09/904,090
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 60/217,583
; PRIOR FILING DATE: 2000-07-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human fragment of thrombin
US-10-050-611-1

Query Match      100.0%; Score 21; DB 13; Length 4;
Best Local Similarity 100.0%; Pred. No. 9.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RGDA 4
        ||||
Db      1 RGDA 4

RESULT 7
US-10-050-688-3
; Sequence 3, Application US/10050688
; Publication No. US20020198154A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; APPLICANT: Crowther, Roger S.
; APPLICANT: Stierberg, Janet
; APPLICANT: Bergmann, John
; TITLE OF INVENTION: STIMULATION OF CARTILAGE GROWTH WITH
; TITLE OF INVENTION: AGONISTS OF THE NON-PROTEOLYTICALLY ACTIVATED THROMBIN
; TITLE OF INVENTION: RECEPTOR
; FILE REFERENCE: 3033.1003-004
; CURRENT APPLICATION NUMBER: US/10/050,688
; CURRENT FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: 09/909,348
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/219,800
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3

; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide fragment of thrombin
US-10-050-688-3

Query Match      100.0%; Score 21; DB 13; Length 4;
Best Local Similarity 100.0%; Pred. No. 9.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RGDA 4
        ||||
Db      1 RGDA 4

RESULT 8
US-10-200-879-23
; Sequence 23, Application US/10200879
; Publication No. US20030144230A1
; GENERAL INFORMATION:
; APPLICANT: HAWLEY-NELSON, PAMELA
; APPLICANT: SHIH, POJEN
; APPLICANT: LAN, JIANQING
; APPLICANT: JESSE, JOEL A.
; APPLICANT: SCHIFFERLI, KEVIN P.
; APPLICANT: GEBYERHU, GULILAT
; TITLE OF INVENTION: PEPTIDE-ENHANCED TRANSFECTIONS
; NUMBER OF SEQUENCES: 120
; CORRESPONDENCE ADDRESS:
; ADDRESS: GREENLEE, WINNER & SULLIVAN
; STREET: 5370 MANHATTAN CIRCLE, SUITE 201
; CITY: BOULDER
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/200,879
; FILING DATE: 23-Jul-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/911,569
; FILING DATE: 23-JUL-2001
; APPLICATION NUMBER: US 09/039,780
; FILING DATE: 16-MAR-1998
; APPLICATION NUMBER: US 08/818,200
; FILING DATE: 14-MAR-1997
; APPLICATION NUMBER: US 08/658,130
; FILING DATE: 04-JUN-1996
; APPLICATION NUMBER: US 08/477,354
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: SULLIVAN, SALLY A.
; REGISTRATION NUMBER: 32,064
; REFERENCE/DOCKET NUMBER: 32-95E
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303)499-8080
; TELEFAX: (303)499-8089
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
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US-10-200-879-23
Query Match      100.0%; Score 21; DB 14; Length 4;
Best Local Similarity 100.0%; Pred. No. 9.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RGDA 4
      ||||
Db      1 RGDA 4

RESULT 9
US-09-989-789-289
; Sequence 289, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 289
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example ZFP
US-09-989-789-289
Query Match      100.0%; Score 21; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RGDA 4
      ||||
Db      1 RGDA 4

RESULT 10
US-09-989-789-670
; Sequence 670, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 670
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example ZFP
US-09-989-789-670
Query Match      100.0%; Score 21; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RGDA 4
      ||||
Db      1 RGDA 4

RESULT 11
US-09-989-789-671
; Sequence 671, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 671
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example ZFP
US-09-989-789-671
Query Match      100.0%; Score 21; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RGDA 4
      ||||
Db      1 RGDA 4

RESULT 12
US-09-989-789-672
; Sequence 672, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 672
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example ZFP
US-09-989-789-672
Query Match      100.0%; Score 21; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RGDA 4
      ||||
Db      1 RGDA 4

RESULT 13
US-09-989-789-673
; Sequence 673, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 673
; LENGTH: 7
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Search completed: March 18, 2004, 07:24:52
Job time : 11.4762 secs

;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: example ZFP
US-09-989-789-673

Query Match 100.0%; Score 21; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGDA 4
|
|
|
|
Db 1 RGDA 4

RESULT 14
US-09-989-789-674
; Sequence 674, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 674
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example ZFP
US-09-989-789-674

Query Match 100.0%; Score 21; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGDA 4
|
|
|
|
Db 1 RGDA 4

RESULT 15
US-09-989-789-675
; Sequence 675, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 675
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example ZFP
US-09-989-789-675

Query Match 100.0%; Score 21; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGDA 4
|
|
|
|
Db 1 RGDA 4

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 18, 2004, 07:21:00 ; Search time 39 Seconds
(without alignments)
92.958 Million cell updates/sec

Title: US-09-909-348-4

Perfect score: 71

Sequence: 1 RGDACXGDSGGPXY 14

Scoring table: BLOSUM62

Gapop 10.0, Capext 0.5

Searched: 1049977 seqs, 258955339 residues

Total number of hits satisfying chosen parameters: 7224

Minimum DB seq length: 14

Maximum DB seq length: 14

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*
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10: /cgn2_6/prodata/1/pubpaa/US09B_PUBCOMB.pep:*
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17: /cgn2_6/prodata/1/pubpaa/US10E_PUBCOMB.pep:*
18: /cgn2_6/prodata/1/pubpaa/US10F_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	67	94.4	14	9	US-09-909-122-4
2	67	94.4	14	13	US-10-050-692-4
3	67	94.4	14	13	US-10-050-688-4
4	52	73.2	14	9	US-09-885-441-6
5	32	45.1	14	10	US-09-300-425B-20
6	32	45.1	14	14	US-10-321-558-31
7	30	42.0	14	15	US-10-341-979-8
8	27	38.0	14	10	US-09-880-748-3215
9	25	35.2	14	9	US-09-815-837-109
10	25	35.2	14	10	US-09-852-455-34
11	25	35.2	14	10	US-09-852-455-35
12	25	35.2	14	10	US-09-852-455-36
13	25	35.2	14	10	US-09-852-455-37
14	25	35.2	14	10	US-09-852-455-38
15	25	35.2	14	10	US-09-880-748-3218

Sequence 16, Appl
Sequence 10, Appl
Sequence 170, Appl
Sequence 173, Appl
Sequence 92, Appl
Sequence 195, Appl
Sequence 23, Appl
Sequence 23, Appl
Sequence 33, Appl
Sequence 8, Appl
Sequence 14, Appl
Sequence 13, Appl
Sequence 188, Appl
Sequence 97, Appl
Sequence 1017, Appl
Sequence 84, Appl
Sequence 320, Appl
Sequence 11, Appl
Sequence 77, Appl
Sequence 108, Appl
Sequence 29, Appl
Sequence 16, Appl
Sequence 158, Appl
Sequence 63, Appl
Sequence 1, Appl
Sequence 5, Appl
Sequence 123, Appl
Sequence 9, Appl

ALIGNMENTS

RESULT 1

US-09-909-122-4
; Sequence 4, Application US/09909122
; Patent No. US20020128202A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; APPLICANT: Crowther, Roger S.
; APPLICANT: Simmons, David J.
; APPLICANT: Yang, Jiping
; APPLICANT: Redin, William R.
; TITLE OF INVENTION: Stimulation Of Bone Growth With Thrombin
; TITLE OF INVENTION: Peptide Derivatives
; FILE REFERENCE: 3033.1002-001
; CURRENT APPLICATION NUMBER: US/09/909,122
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/219,300
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide fragment of Thrombin
; NAME/KEY: VARIANT
; LOCATION: (1)-(14)
; OTHER INFORMATION: Xaa at position six is Glu or Gln
; OTHER INFORMATION: Xaa at position thirteen is Phe, Met, Leu, His or Val
US-09-909-122-4

Query Match 94.4%; Score 67; DB 9; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00088;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGDACXGDSGGPXY 14

DB 1 RGDACXGDSGGPXY 14

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RESULT 2
US-10-050-692-4
; Sequence 4, Application US/10050692
; Publication No. US20020182205A1
; GENERAL INFORMATION:
; APPLICANT: Garney, Darrell H.
; APPLICANT: Crowther, Roger S.
; APPLICANT: Simmons, David J.
; APPLICANT: Yang, Jinping
; APPLICANT: Redin, William R.
; TITLE OF INVENTION: STIMULATION OF BONE GROWTH WITH THROMBIN
; FILE OF INVENTION: PEPTIDE DERIVATIVES
; FILE REFERENCE: 3033.1002-004
; CURRENT APPLICATION NUMBER: US/10/050,692
; PRIOR FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: 09/909,122
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/219,300
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fragment of human prothrombin
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (6)...(6)
; OTHER INFORMATION: xaa = Glu or Gln
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (13)...(13)
; OTHER INFORMATION: xaa = Phe, Met, Leu, His or Val
US-10-050-692-4
; Query Match          94.4%; Score 67; DB 13; Length 14;
; Best Local Similarity 100.0%; Pred. No. 0.00088;
; Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RGDACXGDSGGPKV 14
      |||||
Db      1 RGDACXGDSGGPKV 14

RESULT 3
US-10-050-688-4
; Sequence 4, Application US/10050688
; Publication No. US20020198154A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; APPLICANT: Crowther, Roger S.
; APPLICANT: Stierberg, Janet
; APPLICANT: Bergmann, John
; TITLE OF INVENTION: STIMULATION OF CARTILAGE GROWTH WITH
; FILE OF INVENTION: AGONISTS OF THE NON-PROTEOLYTICALLY ACTIVATED THROMBIN
; FILE REFERENCE: 3033.1003-004
; CURRENT APPLICATION NUMBER: US/10/050,688
; CURRENT FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: 09/909,348
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/219,800
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: BLOCKS domain
US-09-885-441-6
; Sequence 6, Application US/09885441
; Patent No. US20020146407A1
; GENERAL INFORMATION:
; APPLICANT: Xiao, Yonghong
; TITLE OF INVENTION: Regulation of Human Eosinophil Serine
; FILE REFERENCE: 04974.00512
; CURRENT APPLICATION NUMBER: US/09/885,441
; CURRENT FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/212,844
; PRIOR FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: US 60/244,171
; PRIOR FILING DATE: 2000-10-31
; PRIOR APPLICATION NUMBER: US 60/279,766
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: PCT/
; PRIOR FILING DATE: 2001-06-20
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: BLOCKS domain
US-09-885-441-6
; Query Match          73.2%; Score 52; DB 9; Length 14;
; Best Local Similarity 75.0%; Pred. No. 0.18;
; Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      3 DACXGDSGGPKV 14
      |||||
Db      2 DTCKGDSGGPLV 13

RESULT 5
US-09-300-425B-20
; Sequence 20, Application US/09300425B
; Publication No. US20030045681A1
; GENERAL INFORMATION:
; APPLICANT: NERI, Dario
; APPLICANT: TARLI, Lorenzo
; APPLICANT: VITI, Francesca
; APPLICANT: BIRCHER, Manfred
; TITLE OF INVENTION: SPECIFIC BINDING MOLECULES FOR SCINTIGRAPHY, CONJUGATES
; FILE OF INVENTION: CONTAINING THEM AND THERAPEUTIC METHOD FOR TREATMENT OF
; FILE REFERENCE: SCH-1733P1
; CURRENT APPLICATION NUMBER: US/09/300,425B
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; FEATURE:
; OTHER INFORMATION: peptide fragment of thrombin
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (6)...(6)
; OTHER INFORMATION: xaa = Glu or Gln
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (13)...(13)
; OTHER INFORMATION: xaa = Phe, Met, Leu, His or Val
US-10-050-688-4
; Query Match          94.4%; Score 67; DB 13; Length 14;
; Best Local Similarity 100.0%; Pred. No. 0.00088;
; Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RGDACXGDSGGPKV 14
      |||||
Db      1 RGDACXGDSGGPKV 14

RESULT 4
US-09-885-441-6
; Sequence 6, Application US/09885441
; Patent No. US20020146407A1
; GENERAL INFORMATION:
; APPLICANT: Xiao, Yonghong
; TITLE OF INVENTION: Regulation of Human Eosinophil Serine
; FILE REFERENCE: 04974.00512
; CURRENT APPLICATION NUMBER: US/09/885,441
; CURRENT FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/212,844
; PRIOR FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: US 60/244,171
; PRIOR FILING DATE: 2000-10-31
; PRIOR APPLICATION NUMBER: US 60/279,766
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: PCT/
; PRIOR FILING DATE: 2001-06-20
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: BLOCKS domain
US-09-885-441-6
; Query Match          73.2%; Score 52; DB 9; Length 14;
; Best Local Similarity 75.0%; Pred. No. 0.18;
; Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      3 DACXGDSGGPKV 14
      |||||
Db      2 DTCKGDSGGPLV 13

RESULT 5
US-09-300-425B-20
; Sequence 20, Application US/09300425B
; Publication No. US20030045681A1
; GENERAL INFORMATION:
; APPLICANT: NERI, Dario
; APPLICANT: TARLI, Lorenzo
; APPLICANT: VITI, Francesca
; APPLICANT: BIRCHER, Manfred
; TITLE OF INVENTION: SPECIFIC BINDING MOLECULES FOR SCINTIGRAPHY, CONJUGATES
; FILE OF INVENTION: CONTAINING THEM AND THERAPEUTIC METHOD FOR TREATMENT OF
; FILE REFERENCE: SCH-1733P1
; CURRENT APPLICATION NUMBER: US/09/300,425B
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; CURRENT FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: 09/075,338
; PRIOR FILING DATE: 1998-05-11
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: antibody linker
US-09-300-425B-20

Query Match          45.1%; Score 32; DB 10; Length 14;
Best Local Similarity 60.0%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GDACXGDSGG 11
DB 1 GDGSSGGSGG 10

RESULT 6
US-10-321-558-31
; Sequence 31, Application US/10321558
; Publication No. US2003017663A1
; GENERAL INFORMATION:
; APPLICANT: NERI, DARIO
; APPLICANT: TARLI, LORENZO
; APPLICANT: VITI, FRANCESCA
; APPLICANT: BIRCHLER, MANFRED
; TITLE OF INVENTION: SPECIFIC BINDING MOLECULES FOR SCINTIGRAPHY
; FILE REFERENCE: NOTAR-1 C1
; CURRENT APPLICATION NUMBER: US/10/321,558
; PRIOR FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: 09/512,082
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 09/300,425
; PRIOR FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: 09/075,338
; PRIOR FILING DATE: 1998-05-11
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: linker sequence
US-10-321-558-31

Query Match          45.1%; Score 32; DB 14; Length 14;
Best Local Similarity 60.0%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GDACXGDSGG 11
DB 1 GDGSSGGSGG 10

RESULT 7
US-10-341-979-8
; Sequence 8, Application US/10341979
; Publication No. US20040002128A1
; GENERAL INFORMATION:
; APPLICANT: Hong Kong University of Science & Technology
; APPLICANT: Chang, Donald Choy
; APPLICANT: Luo, Qian Kathy
; TITLE OF INVENTION: GFP-BASED METHODS FOR DETECTING APOPTOSIS
; FILE REFERENCE: 32144183-1
; CURRENT APPLICATION NUMBER: US/10/341,979
; CURRENT FILING DATE: 2003-01-11
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; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 14
; TYPE: PRT
; ORGANISM: mammalian
US-10-341-979-8

Query Match          42.3%; Score 30; DB 15; Length 14;
Best Local Similarity 60.0%; Pred. No. 4.1e+02;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GDACXGDSGG 11
DB 5 GDEVDGSGG 14

RESULT 8
US-09-880-748-3215
; Sequence 3215, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3215
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-3215

Query Match          38.0%; Score 27; DB 10; Length 14;
Best Local Similarity 83.3%; Pred. No. 1.2e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GDSGGP 12
DB 7 GDSGGP 12

RESULT 9
US-09-815-837-109
; Sequence 109, Application US/09815837
; Patent No. US2002008241A1
; GENERAL INFORMATION:
; APPLICANT: Carter, Barrick
; APPLICANT: Zhu, Shirley
; APPLICANT: Arimilli, Subhashini
; APPLICANT: Wang, Aljun
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Immune Medators and Related Methods
; FILE REFERENCE: 014058-00567005
; CURRENT APPLICATION NUMBER: US/09/815,837
; CURRENT FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: US 60/191,274
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: US 60/204,249
; PRIOR FILING DATE: 2000-05-15
; PRIOR APPLICATION NUMBER: US 60/264,003
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; PRIOR FILING DATE: 2001-01-23
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 109
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Cavia porcellus
US-09-852-455-35

Query Match      35.2%; Score 25; DB 10; Length 14;
Best Local Similarity 66.7%; Pred. No. 2.4e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      7 GDSGGP 12
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Db      1 GELGGP 6

RESULT 12
US-09-852-455-36
; Sequence 36, Application US/09852455
; Publication No. US20030054348A1
; GENERAL INFORMATION:
; APPLICANT: BLUME, ARTHUR J.
; APPLICANT: GOLDSTEIN, NEIL
; APPLICANT: PILLUTA, RENUKA
; APPLICANT: HSIAO, KU-CHUAN
; APPLICANT: PRENDERGAST, JOHN
; TITLE OF INVENTION: METHODS OF IDENTIFYING THE ACTIVITY OF GENE PRODUCTS
; FILE REFERENCE: 2598-4004US1
; CURRENT APPLICATION NUMBER: US/09/852,455
; CURRENT FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: 60/202,912
; PRIOR FILING DATE: 2000-05-09
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-852-455-36

Query Match      35.2%; Score 25; DB 10; Length 14;
Best Local Similarity 66.7%; Pred. No. 2.4e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      7 GDSGGP 12
      |: |||
Db      1 GELGGP 6

RESULT 13
US-09-852-455-37
; Sequence 37, Application US/09852455
; Publication No. US20030054348A1
; GENERAL INFORMATION:
; APPLICANT: BLUME, ARTHUR J.
; APPLICANT: GOLDSTEIN, NEIL
; APPLICANT: PILLUTA, RENUKA
; APPLICANT: HSIAO, KU-CHUAN
; APPLICANT: PRENDERGAST, JOHN
; TITLE OF INVENTION: METHODS OF IDENTIFYING THE ACTIVITY OF GENE PRODUCTS
; FILE REFERENCE: 2598-4004US1
; CURRENT APPLICATION NUMBER: US/09/852,455
; CURRENT FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: 60/202,912
; PRIOR FILING DATE: 2000-05-09
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 37
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-852-455-37

Query Match      35.2%; Score 25; DB 10; Length 14;
Best Local Similarity 66.7%; Pred. No. 2.4e+03;
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; PRIOR FILING DATE: 2001-01-23
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 109
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:downstream
; OTHER INFORMATION: linker for COS80 and COS87
US-09-815-837-109

Query Match      35.2%; Score 25; DB 9; Length 14;
Best Local Similarity 66.7%; Pred. No. 2.4e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      7 GDSGGP 12
      |: |||
Db      7 GSGGGP 12

RESULT 10
US-09-852-455-34
; Sequence 34, Application US/09852455
; Publication No. US20030054348A1
; GENERAL INFORMATION:
; APPLICANT: BLUME, ARTHUR J.
; APPLICANT: GOLDSTEIN, NEIL
; APPLICANT: PILLUTA, RENUKA
; APPLICANT: HSIAO, KU-CHUAN
; APPLICANT: PRENDERGAST, JOHN
; TITLE OF INVENTION: METHODS OF IDENTIFYING THE ACTIVITY OF GENE PRODUCTS
; FILE REFERENCE: 2598-4004US1
; CURRENT APPLICATION NUMBER: US/09/852,455
; CURRENT FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: 60/202,912
; PRIOR FILING DATE: 2000-05-09
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Bos taurus
US-09-852-455-34

Query Match      35.2%; Score 25; DB 10; Length 14;
Best Local Similarity 66.7%; Pred. No. 2.4e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      7 GDSGGP 12
      |: |||
Db      1 GELGGP 6

RESULT 11
US-09-852-455-35
; Sequence 35, Application US/09852455
; Publication No. US20030054348A1
; GENERAL INFORMATION:
; APPLICANT: BLUME, ARTHUR J.
; APPLICANT: GOLDSTEIN, NEIL
; APPLICANT: PILLUTA, RENUKA
; APPLICANT: HSIAO, KU-CHUAN
; APPLICANT: PRENDERGAST, JOHN
; TITLE OF INVENTION: METHODS OF IDENTIFYING THE ACTIVITY OF GENE PRODUCTS
; FILE REFERENCE: 2598-4004US1
; CURRENT APPLICATION NUMBER: US/09/852,455
; CURRENT FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: 60/202,912
; PRIOR FILING DATE: 2000-05-09
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
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Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GDSGGP 12
| : |||
Db 1 GELGGP 6

Db 2 REPADYGDYG 11
| : |||

Search completed: March 18, 2004, 07:27:53
Job time : 40 secs

RESULT 14
US-09-852-455-38
; Sequence 38, Application US/09852455
; Publication No. US20030054348A1
; GENERAL INFORMATION:
; APPLICANT: BLUME, ARTHUR J.
; APPLICANT: GOLDSTEIN, NEIL
; APPLICANT: PILLUTA, RENUKA
; APPLICANT: HSIAO, KU-CHUAN
; APPLICANT: PRENDERGAST, JOHN
; TITLE OF INVENTION: METHODS OF IDENTIFYING THE ACTIVITY OF GENE PRODUCTS
; FILE REFERENCE: 2598-4004US1
; CURRENT APPLICATION NUMBER: US/09/852,455
; CURRENT FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: 60/202,912
; PRIOR FILING DATE: 2000-05-09
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Felis catus
US-09-852-455-38

Query Match 35.2%; Score 25; DB 10; Length 14;
Best Local Similarity 66.7%; Pred. No. 2.4e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GDSGGP 12
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Db 1 GELGGP 6

RESULT 15
US-09-880-748-3218
; Sequence 3218, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3218
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-3218

Query Match 35.2%; Score 25; DB 10; Length 14;
Best Local Similarity 60.0%; Pred. No. 2.4e+03;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RGDACXGDSG 10

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 18, 2004, 07:16:14 ; Search time 36.6667 Seconds
(without alignments)
98.874 Million cell updates/sec

Title: US-09-909-348-4

Perfect score: 71
Sequence: 1 RGDACXGDSGGPXV 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1049977 seqs, 258955339 residues

Total number of hits satisfying chosen parameters: 1049977

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:**

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description
1	67	94.4	14	9	US-09-909-122-4
2	67	94.4	14	13	US-10-050-692-4
3	67	94.4	14	13	US-10-050-688-4
4	67	94.4	23	9	US-09-777-328-8
5	67	94.4	23	9	US-09-904-090-3
6	67	94.4	23	13	US-10-050-692-6
7	67	94.4	23	13	US-10-050-611-3
8	67	94.4	23	13	US-10-050-611-4
9	67	94.4	23	13	US-10-050-688-5
10	67	94.4	23	13	US-10-050-688-6
11	67	94.4	25	9	US-09-903-348-5
12	67	94.4	25	9	US-09-903-122-5
13	67	94.4	25	13	US-10-050-692-5
14	67	94.4	250	10	US-09-898-837A-45
15	67	94.4	251	10	US-09-898-837A-41

16	67	94.4	259	15	US-10-165-442-2	Sequence 2, Appli
17	67	94.4	259	15	US-10-165-442-4	Sequence 4, Appli
18	67	94.4	295	15	US-10-165-442-1	Sequence 1, Appli
19	67	94.4	295	15	US-10-165-442-3	Sequence 3, Appli
20	67	94.4	622	14	US-10-020-141-8	Sequence 8, Appli
21	67	94.4	622	14	US-10-017-631-2	Sequence 2, Appli
22	67	94.4	622	14	US-10-214-932-116	Sequence 116, App
23	67	94.4	622	14	US-10-172-712-29	Sequence 29, Appl
24	61	85.9	30	9	US-09-820-893-111	Sequence 111, App
25	61	85.9	30	12	US-10-607-565-111	Sequence 11, App
26	61	85.9	187	9	US-09-804-156-17	Sequence 17, Appl
27	61	85.9	187	9	US-09-946-633-9	Sequence 9, Appli
28	61	85.9	187	13	US-10-125-459-9	Sequence 9, Appli
29	61	85.9	187	13	US-10-067-761-17	Sequence 17, Appl
30	61	85.9	187	14	US-10-319-519-17	Sequence 17, Appl
31	61	85.9	311	11	US-09-981-151A-75	Sequence 75, Appl
32	61	85.9	414	9	US-09-820-893-69	Sequence 69, Appl
33	61	85.9	414	12	US-10-607-565-69	Sequence 69, Appl
34	61	85.9	418	11	US-09-981-151A-29	Sequence 29, Appl
35	61	85.9	445	11	US-09-981-151A-73	Sequence 73, Appl
36	61	85.9	455	11	US-09-981-151A-72	Sequence 72, Appl
37	61	85.9	457	9	US-09-888-615-110	Sequence 110, App
38	61	85.9	457	11	US-09-981-151A-71	Sequence 71, Appl
39	61	85.9	472	11	US-09-981-151A-27	Sequence 27, Appl
40	61	85.9	480	9	US-09-820-893-108	Sequence 108, App
41	61	85.9	480	12	US-10-607-565-108	Sequence 108, App
42	59	83.1	415	12	US-10-670-628-2	Sequence 2, Appli
43	59	83.1	419	10	US-09-978-317A-4	Sequence 4, Appli
44	59	83.1	419	14	US-10-182-263-1	Sequence 1, Appli
45	59	83.1	419	14	US-10-182-263-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-09-909-122-4
; Sequence 4, Application US/09909122
; Patent No. US20020128202A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; APPLICANT: Crowther, Roger S.
; APPLICANT: Simmons, David J.
; APPLICANT: Yang, Jinping
; APPLICANT: Redin, William R.
; TITLE OF INVENTION: Stimulation Of Bone Growth With Thrombin
; TITLE OF INVENTION: Peptide Derivatives
; FILE REFERENCE: 3039, 1002-001
; CURRENT APPLICATION NUMBER: US/09/909,122
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/219,300
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide fragment of Thrombin
; NAME/KEY: VARIANT
; LOCATION: (1) (14)
; OTHER INFORMATION: Xaa at position six is Gly or Gln
; OTHER INFORMATION: Xaa at position thirteen is Phe, Met, Leu, His or Val
US-09-909-122-4

Query Match 94.4%; Score 67; DB 9; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00088;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 RGDACXGDSGGPXV 14
Db 1 RGDACXGDSGGPXV 14

FEATURE:
OTHER INFORMATION: peptide fragment of thrombin
FEATURE:
NAME/KEY: VARIANT
LOCATION: (6)....(6)
OTHER INFORMATION: Xaa = Glu or Gln
FEATURE:
NAME/KEY: VARIANT
LOCATION: (13)....(13)
OTHER INFORMATION: Xaa = Phe, Met, Leu, His or Val
US-10-050-688-4
Query Match 94.4%; Score 67; DB 13; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00088;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RGDACXGDSGGPXV 14
DB 1 RGDACXGDSGGPXV 14
RESULT 4
US-09-777-328-8
Sequence 8, Application US/09777328
Patent No. US20020032314A1
GENERAL INFORMATION:
APPLICANT: CAREY, DARRELL H.
APPLICANT: RAMAKRISHNAN, SHYAM
TITLE OF INVENTION: SYNTHETIC PEPTIDE NEUTROPHIL CELL CHEMOTACTIC AGENTS
FILE REFERENCE: CHBP:002
CURRENT APPLICATION NUMBER: US/09/777,328
CURRENT FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: 08/330,594
PRIOR FILING DATE: 1994-10-28
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin ver. 2.0
SEQ ID NO 8
LENGTH: 23
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: Peptide
US-09-777-328-8
Query Match 94.4%; Score 67; DB 9; Length 23;
Best Local Similarity 85.7%; Pred. No. 0.0014;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 RGDACXGDSGGPXV 14
DB 10 RGDACEGDSGGPFV 23
RESULT 5
US-09-904-090-3
Sequence 3, Application US/09904090
Patent No. US20020061852A1
GENERAL INFORMATION:
APPLICANT: Carney, Darrell
TITLE OF INVENTION: METHODS OF THERAPY WITH THROMBIN DERIVED
FILE REFERENCE: 3033.1000-001
CURRENT APPLICATION NUMBER: US/09/904,090
CURRENT FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: US 60/217,583
PRIOR FILING DATE: 2000-07-12
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 23
TYPE: PRT
ORGANISM: Artificial Sequence

US-10-050-692-4
Sequence 4, Application US/10050692
Publication No. US20020182205A1
GENERAL INFORMATION:
APPLICANT: Carney, Darrell H.
APPLICANT: Crowther, Roger S.
APPLICANT: Simmons, David J.
APPLICANT: Yang, Jinping
APPLICANT: Redin, William R.
TITLE OF INVENTION: STIMULATION OF BONE GROWTH WITH THROMBIN
FILE REFERENCE: 3033.1002-004
CURRENT APPLICATION NUMBER: US/10/050,692
CURRENT FILING DATE: 2002-01-16
PRIOR APPLICATION NUMBER: 09/909,122
PRIOR FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: 60/219,300
PRIOR FILING DATE: 2000-07-19
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 14
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: fragment of human prothrombin
FEATURE:
NAME/KEY: VARIANT
LOCATION: (6)....(6)
OTHER INFORMATION: Xaa = Glu or Gln
FEATURE:
NAME/KEY: VARIANT
LOCATION: (13)....(13)
OTHER INFORMATION: Xaa = Phe, Met, Leu, His or Val
US-10-050-692-4
Query Match 94.4%; Score 67; DB 13; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00088;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RGDACXGDSGGPXV 14
DB 1 RGDACXGDSGGPXV 14
RESULT 3
US-10-050-688-4
Sequence 4, Application US/10050688
Publication No. US20020198154A1
GENERAL INFORMATION:
APPLICANT: Carney, Darrell H.
APPLICANT: Crowther, Roger S.
APPLICANT: Stierberg, Janet
APPLICANT: Bergmann, John
TITLE OF INVENTION: STIMULATION OF CARTILAGE GROWTH WITH
FILE REFERENCE: 3033.1003-004
CURRENT APPLICATION NUMBER: US/10/050,688
CURRENT FILING DATE: 2002-01-16
PRIOR APPLICATION NUMBER: 09/909,348
PRIOR FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: 60/219,800
PRIOR FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 14
TYPE: PRT
ORGANISM: Artificial Sequence

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RESULT 7
US10-050-611-3
; Sequence 3, Application US/10050611
; Publication No. US20020187933A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; TITLE OF INVENTION: METHODS OF THERAPY WITH
; TITLE OF INVENTION: PEPTIDES
; FILE REFERENCE: 3033.1000-008
; CURRENT APPLICATION NUMBER: US/10/050,611
; CURRENT FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: 09/904,090
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 67/217,583
; PRIOR FILING DATE: 2000-07-12
; NUMBER OF SEQ IDS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3

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RESULT 9
US 10-050-688-5
; Sequence 5, Application US/10050688
; Publication No. US20020198154A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; APPLICANT: Crowther, Roger S.
; APPLICANT: Stiernberg, Janet
; APPLICANT: Bergmann, John
; TITLE OF INVENTION: STIMULATION OF CARTILAGE GROWTH WITH
; TITLE OF INVENTION: AGONISTS OF THE NON-PROTEOLYTICALLY ACTIVATED THROMBIN
; TITLE OF INVENTION: RECEPTOR
; FILE REFERENCE: 3033.1003-004
; CURRENT APPLICATION NUMBER: US/10/050,688
; CURRENT FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: 09/909,348
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/219,800
; PRIOR FILING DATE: 2000-07-20

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; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide fragment of thrombin
US-10-050-688-5

Query Match          94.4%; Score 67; DB 13; Length 23;
Best Local Similarity 85.7%; Pred. No. 0.0014;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RGDACXGDSGGP XV 14
Db 10 RGDACEGDSGGP XV 23

RESULT 10
US-10-050-688-6
; Sequence 6, Application US/10050688
; Publication No. US20020198154A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; APPLICANT: Crowther, Roger S.
; APPLICANT: Stierberg, Janet
; APPLICANT: Bergmann, John
; TITLE OF INVENTION: STIMULATION OF CARTILAGE GROWTH WITH
; TITLE OF INVENTION: AGONISTS OF THE NON-PROTEOLYTICALLY ACTIVATED THROMBIN
; TITLE OF INVENTION: RECEPTOR
; FILE REFERENCE: 3033.1003-004
; CURRENT APPLICATION NUMBER: US/10/050,688
; PRIOR FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: 09/909,348
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/219,800
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide fragment of thrombin
; NAME/KEY: AMIDATION
; LOCATION: (23)...(23)
; OTHER INFORMATION: CONH2
US-10-050-688-6

Query Match          94.4%; Score 67; DB 13; Length 23;
Best Local Similarity 85.7%; Pred. No. 0.0014;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RGDACXGDSGGP XV 14
Db 10 RGDACEGDSGGP XV 23

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US-09-909-348-5
; Sequence 5, Application US/09909348
; Patent No. US20020042373A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; APPLICANT: Crowther, Roger S.
; APPLICANT: Stierberg, Janet
; APPLICANT: Bergmann, John
; TITLE OF INVENTION: Stimulation Of Cartilage Growth With Agonists
; TITLE OF INVENTION: Of The No. US20020042373A1-Proteolytically Activated Thrombin Re
; FILE REFERENCE: 3033.1003-001
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; CURRENT APPLICATION NUMBER: US/09/909,348
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/219,800
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide fragment of Thrombin
US-09-909-348-5

Query Match          94.4%; Score 67; DB 9; Length 25;
Best Local Similarity 85.7%; Pred. No. 0.0015;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RGDACXGDSGGP XV 14
Db 12 RGDACEGDSGGP XV 25

RESULT 12
US-09-909-122-5
; Sequence 5, Application US/09909122
; Patent No. US20020128202A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; APPLICANT: Crowther, Roger S.
; APPLICANT: Simmons, David J.
; APPLICANT: Yang, Jinping
; APPLICANT: Redin, William R.
; TITLE OF INVENTION: Stimulation Of Bone Growth With Thrombin
; TITLE OF INVENTION: Peptide Derivatives
; FILE REFERENCE: 3033.1002-001
; CURRENT APPLICATION NUMBER: US/09/909,122
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/219,300
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide fragment of Thrombin
US-09-909-122-5

Query Match          94.4%; Score 67; DB 9; Length 25;
Best Local Similarity 85.7%; Pred. No. 0.0015;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RGDACXGDSGGP XV 14
Db 12 RGDACEGDSGGP XV 25

RESULT 13
US-10-050-692-5
; Sequence 5, Application US/10050692
; Publication No. US20020182205A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; APPLICANT: Crowther, Roger S.
; APPLICANT: Simmons, David J.
; APPLICANT: Yang, Jinping
; APPLICANT: Redin, William R.
; TITLE OF INVENTION: STIMULATION OF BONE GROWTH WITH THROMBIN
; TITLE OF INVENTION: PEPTIDE DERIVATIVES
; FILE REFERENCE: 3033.1002-004
; CURRENT APPLICATION NUMBER: US/10/050,692
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Best Local Similarity 85.7%; Pred. No. 0.014; Mismatches 0; Gaps 0;
Matches 12; Conservative 0; Indels 2; Gaps 0;

QY 1 RGDACXGDSGGPXV 14
DB 197 RGDACEGDSGGPFV 210

RESULT 15
US-09-898-837A-41
; Sequence 41, Application US/09898837A
; Publication No. US2003007697A1
; GENERAL INFORMATION:
; APPLICANT: Quinn, Kerry E.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Majumder, Kumud
; APPLICANT: Vernet, Corine
; APPLICANT: Herrmann, John L.
; APPLICANT: Burgess, Catherine
; APPLICANT: Fernandes, Elma
; APPLICANT: Taupier Jr., Raymond
; APPLICANT: Rastelli, Luca
; APPLICANT: Curagen Corporation
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: MacDougall, John R.
; TITLE OF INVENTION: NOVEL SERINE/THREONINE PROTEIN-KINASE LIKE PROTEINS AND
; FILE REFERENCE: 15966-598 CIP
; CURRENT APPLICATION NUMBER: US/09/898,837A
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/165,986
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/194,839
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/195,637
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/197,080
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/232,677
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/181,347
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/194,195
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/215,906
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: U.S.S.N. 09/715,427
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Bos taurus
; US-09-898-837A-41

Query Match 94.4%; Score 67; DB 10; Length 251;
Best Local Similarity 85.7%; Pred. No. 0.014; Mismatches 0; Gaps 0;
Matches 12; Conservative 0; Indels 2; Gaps 0;

QY 1 RGDACXGDSGGPXV 14
DB 198 RGDACEGDSGGPFV 211

Search completed: March 18, 2004, 07:24:52
Job time : 36.6667 secs

CURRENT FILING DATE: 2002-01-16
PRIOR APPLICATION NUMBER: 09/909,122
PRIOR FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: 60/219,300
PRIOR FILING DATE: 2000-07-19
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 25
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: fragment of human prothrombin
US-10-050-692-5

Query Match 94.4%; Score 67; DB 13; Length 25;
Best Local Similarity 85.7%; Pred. No. 0.0015; Mismatches 0; Gaps 0;
Matches 12; Conservative 0; Indels 2; Gaps 0;

QY 1 RGDACXGDSGGPXV 14
DB 12 RGDACEGDSGGPFV 25

RESULT 14
US-09-898-837A-45
; Sequence 45, Application US/09898837A
; Publication No. US2003007697A1
; GENERAL INFORMATION:
; APPLICANT: Quinn, Kerry E.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Majumder, Kumud
; APPLICANT: Vernet, Corine
; APPLICANT: Herrmann, John L.
; APPLICANT: Burgess, Catherine
; APPLICANT: Fernandes, Elma
; APPLICANT: Taupier Jr., Raymond
; APPLICANT: Rastelli, Luca
; APPLICANT: Curagen Corporation
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: MacDougall, John R.
; TITLE OF INVENTION: NOVEL SERINE/THREONINE PROTEIN-KINASE LIKE PROTEINS AND
; FILE REFERENCE: 15966-598 CIP
; CURRENT APPLICATION NUMBER: US/09/898,837A
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/165,986
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/194,839
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/195,637
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/197,080
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/232,677
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/181,347
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/194,195
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/215,906
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: U.S.S.N. 09/715,427
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 45
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Bos taurus
; US-09-898-837A-45

Query Match 94.4%; Score 67; DB 10; Length 250;

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OM protein - protein search, using sw model

Run on: March 18, 2004, 07:22:05 ; Search time 39 Seconds
(without alignments)
165.997 Million cell updates/sec

Title: US-09-909-348-5

Perfect score: 141

Sequence: 1 AGTRYKDEKRGDACEGDSGGPFV 25

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1049977 seqs, 25895339 residues

Total number of hits satisfying chosen parameters: 2971

Minimum DB seq length: 25

Maximum DB seq length: 25

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09D_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	141	100.0	25	9	US-09-909-122-5
3	141	100.0	25	13	US-10-050-632-5
4	38	27.0	25	15	US-10-353-522A-1
5	36	25.5	25	9	US-09-864-761-37498
6	33	23.4	25	9	US-09-864-761-43492
7	31.5	22.3	25	14	US-10-280-066-233
8	31	22.0	25	10	US-09-852-455-75
9	31	22.0	25	10	US-09-962-756-1099
10	31	22.0	25	14	US-10-133-128-205
11	31	22.0	25	14	US-10-289-660-205
12	31	22.0	25	15	US-10-253-471-1099
13	31	22.0	25	16	US-10-253-493-1099
14	30	21.3	25	10	US-09-933-767-598
15	30	21.3	25	13	US-10-036-869-7

Sequence 538, App
Sequence 11, Appl
Sequence 409, App
Sequence 45944, A
Sequence 255, App
Sequence 219, App
Sequence 23, Appl
Sequence 3, Appl
Sequence 256, App
Sequence 3, Appl
Sequence 32, Appl
Sequence 311, App
Sequence 312, App
Sequence 314, App
Sequence 31, Appl
Sequence 45572, A
Sequence 322, App
Sequence 263, App
Sequence 362, App
Sequence 118, App
Sequence 28, Appl
Sequence 31, Appl
Sequence 4, Appl
Sequence 31, Appl
Sequence 362, App
Sequence 26, Appl
Sequence 16, Appl
Sequence 313, App
Sequence 119, App

ALIGNMENTS

RESULT 1

US-09-909-348-5
; Sequence 5, Application US/09909348
; Patent No. US20020042373A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; APPLICANT: Crowther, Roger S.
; APPLICANT: Stierberg, Janet
; APPLICANT: Bergmann, John
; TITLE OF INVENTION: Stimulation Of Cartilage Growth With Agonists
; FILE OF INVENTION: Of The No. US20020042373A1-Proteolytically Activated Thrombin Re
; FILE REFERENCE: 3033.1003-001
; CURRENT APPLICATION NUMBER: US/09/909,348
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/219,800
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide fragment of Thrombin
US-09-909-348-5

Query Match 100.0%; Score 141; DB 9; Length 25;
Best Local Similarity 100.0%; Pred.No. 6.2e-12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Ov 1 AGTRYKDEKRGDACEGDSGGPFV 25

Db 1 AGTRYKDEKRGDACEGDSGGPFV 25

RESULT 2

US-09-909-122-5
; Sequence 5, Application US/09909122

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; Patent No. US20020128202A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; APPLICANT: Crowther, Roger S.
; APPLICANT: Simmons, David J.
; APPLICANT: Yang, Jinping
; APPLICANT: Redin, William R.
; TITLE OF INVENTION: Stimulation Of Bone Growth With Thrombin
; FILE REFERENCE: 3033.1002-001
; CURRENT APPLICATION NUMBER: US/09/909,122
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/219,300
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide fragment of Thrombin
US-09-909-122-5

Query Match      100.0%; Score 141; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 6.2e-12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGTRYKPDGKRGDACEGDSGGPFV 25
Db 1 AGTRYKPDGKRGDACEGDSGGPFV 25

RESULT 3
US-10-050-692-5
; Sequence 5 Application US/10050692
; Publication No. US20020182205A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; APPLICANT: Crowther, Roger S.
; APPLICANT: Simmons, David J.
; APPLICANT: Yang, Jinping
; APPLICANT: Redin, William R.
; TITLE OF INVENTION: STIMULATION OF BONE GROWTH WITH THROMBIN
; FILE REFERENCE: 3033.1002-004
; CURRENT APPLICATION NUMBER: US/10/050,692
; CURRENT FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: 09/909,122
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/219,300
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fragment of human prothrombin
US-10-050-692-5

Query Match      100.0%; Score 141; DB 13; Length 25;
Best Local Similarity 100.0%; Pred. No. 6.2e-12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGTRYKPDGKRGDACEGDSGGPFV 25
Db 1 AGTRYKPDGKRGDACEGDSGGPFV 25

RESULT 4
US-10-353-522A-1
; Sequence 1 Application US/10353522A
; Publication No. US20030216296A1
; GENERAL INFORMATION:
; APPLICANT: Welsch Pharmaceuticals, Inc.
; APPLICANT: Park, Jong-Gu
; APPLICANT: Moon, Ik-Jae
; APPLICANT: Kim, Young-Cheol
; TITLE OF INVENTION: Peptide for Increasing Transfection Efficiency
; FILE REFERENCE: 57354-13USA
; CURRENT APPLICATION NUMBER: US/10/353,522A
; CURRENT FILING DATE: 2003-01-28
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 25
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: RGD-RGD-TatC-RGD-RGD
US-10-353-522A-1

Query Match      27.0%; Score 38; DB 15; Length 25;
Best Local Similarity 40.0%; Pred. No. 3.2e+02;
Matches 8; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

Qy 2 GTRYKPDGKRGDACEGDSG 21
Db 5 GDRKRRQRRRPPQCRGDRG 24

RESULT 5
US-03-864-761-37498
; Sequence 37498 Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Ascmica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
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;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: US 60/234,687
;; PRIOR FILING DATE: 2000-09-21
;; PRIOR APPLICATION NUMBER: US 09/608,408
;; PRIOR FILING DATE: 2000-06-30
;; PRIOR APPLICATION NUMBER: US 09/774,203
;; PRIOR FILING DATE: 2001-01-29
;; NUMBER OF SEQ ID NOS: 49117
;; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
;; SEQ ID NO 37498
;; LENGTH: 25
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: MAP TO AC011504.2
;; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 10
;; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 9
;; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 10
;; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 8.6
;; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 9.1
;; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 11
;; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 8.9
;; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 10
;; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 10
;; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 9.5
;; OTHER INFORMATION: SWISSPROT HIT: P22857, EVALUATE 1.70e+00
;; US-09-864-761-37498

Query Match 25.5%; Score 36; DB 9; Length 25;
Best Local Similarity 66.7%; Pred. No. 5.9e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0;

Oy 15 ACEGDSGGP 23

Db 11 ACQSRSGGP 19

RESULT 6
US-09-864-761-43492
;; Sequence 43492, Application US/09864761
;; Patent No. US20020048763A1
;; GENERAL INFORMATION:
;; APPLICANT: Penn, Sharon G.
;; APPLICANT: Rank, David R.
;; APPLICANT: Hanzel, David K.
;; APPLICANT: Chen, Wensheng
;; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
;; FILE REFERENCE: Aeomica-X-1
;; CURRENT APPLICATION NUMBER: US/09/864,761
;; CURRENT FILING DATE: 2001-05-23
;; PRIOR APPLICATION NUMBER: US 60/180,312
;; PRIOR FILING DATE: 2000-02-04
;; PRIOR APPLICATION NUMBER: US 60/207,456
;; PRIOR FILING DATE: 2000-05-26
;; PRIOR APPLICATION NUMBER: US 09/632,366
;; PRIOR FILING DATE: 2000-08-03
;; PRIOR APPLICATION NUMBER: GB 24263.6
;; PRIOR FILING DATE: 2000-10-04
;; PRIOR APPLICATION NUMBER: US 60/236,359
;; PRIOR FILING DATE: 2000-09-27
;; PRIOR APPLICATION NUMBER: PCT/US01/00666
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00667
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00664
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00669
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00665
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00668
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;; PRIOR APPLICATION NUMBER: PCT/US01/00663
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00662
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00661
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00670
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: US 60/234,687
;; PRIOR FILING DATE: 2000-09-21
;; PRIOR APPLICATION NUMBER: US 09/608,408
;; PRIOR FILING DATE: 2000-06-30
;; PRIOR APPLICATION NUMBER: US 09/774,203
;; PRIOR FILING DATE: 2001-01-29
;; NUMBER OF SEQ ID NOS: 49117
;; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
;; SEQ ID NO 43492
;; LENGTH: 25
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: MAP TO AC006324.2
;; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.6
;; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.72
;; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.8
;; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1
;; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.75
;; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.61
;; US-09-864-761-43492

Query Match 23.4%; Score 33; DB 9; Length 25;
Best Local Similarity 40.0%; Pred. No. 1.5e+03;
Matches 6; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Oy 8 DEKRGDACEGDSGG 22

Db 10 EEGMQGDEPDHNGG 24

RESULT 7
US-10-280-066-233
;; Sequence 233, Application US/10280066
;; Publication No. US20030180718A1
;; GENERAL INFORMATION:
;; APPLICANT: Pillutla, Renuka C.
;; APPLICANT: Brissette, Renee
;; APPLICANT: Spruyt, Michael
;; APPLICANT: Dedova, Olga
;; APPLICANT: Blume, Arthur J.
;; APPLICANT: Prendergast, John
;; APPLICANT: Goldstein, Neil I.
;; TITLE OF INVENTION: TARGET SPECIFIC SCREENING AND ITS USE FOR IDENTIFYING TARGET BINDI
;; FILE REFERENCE: 2598-4009US1
;; CURRENT APPLICATION NUMBER: US/10/280,066
;; CURRENT FILING DATE: 2002-10-24
;; PRIOR APPLICATION NUMBER: 60/345,471
;; PRIOR FILING DATE: 2001-10-24
;; NUMBER OF SEQ ID NOS: 537
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 233
;; LENGTH: 25
;; TYPE: PRT
;; ORGANISM: Eschericia coli
;; FEATURE:
;; NAME/KEY: MISC FEATURE
;; OTHER INFORMATION: 07902-DG12-20M-PP-BC-C5
;; US-10-280-066-233

Query Match 22.3%; Score 31.5; DB 14; Length 25;
Best Local Similarity 52.3%; Pred. No. 2.3e+03;
Matches 9; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

Oy 1 AGTRYKPDGKRGDACE 17

US-09-962-756-1099

Query Match 22.0%; Score 31; DB 10; Length 25;
 Best Local Similarity 57.1%; Pred. No. 2.7e+03;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 18 GDSGGPF 24
 DB 16 GEAGGPF 22

RESULT 10
 US-10-133-128-205
 ; Sequence 205, Application US/10133128
 ; Publication No. US20030082630A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KOLKMAN, JOOST A.
 ; APPLICANT: STEMMER, WILLEM P.C.
 ; TITLE OF INVENTION: COMBINATORIAL LIBRARIES OF MONOMER DOMAINS
 ; FILE REFERENCE: 0319.410US
 ; CURRENT APPLICATION NUMBER: US/10/133,128
 ; CURRENT FILING DATE: 2002-04-26
 ; PRIOR FILING DATE: 2002-04-18
 ; PRIOR APPLICATION NUMBER: 60/374,107
 ; PRIOR FILING DATE: 2001-11-26
 ; PRIOR APPLICATION NUMBER: 60/337,209
 ; PRIOR FILING DATE: 2001-11-19
 ; PRIOR APPLICATION NUMBER: 60/286,823
 ; PRIOR FILING DATE: 2001-04-26
 ; NUMBER OF SEQ ID NOS: 244
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 205
 ; LENGTH: 25
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 ; OTHER INFORMATION: peptide linker
 ; NAME/KEY: misc feature
 ; LOCATION: (1)..(12)
 ; OTHER INFORMATION: This region may vary in length from 1-12 residues,
 ; OTHER INFORMATION: 3-9 residues, 4-8 residues or 4-7 residues
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (14)..(25)
 ; OTHER INFORMATION: This region may vary in length from 1-12 residues,
 ; OTHER INFORMATION: 3-9 residues, 4-8 residues or 4-7 residues
 ; US-10-133-128-205

Query Match 22.0%; Score 31; DB 14; Length 25;
 Best Local Similarity 46.2%; Pred. No. 2.7e+03;
 Matches 6; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 10 GKRGDACEGDSGG 22
 DB 7 GGGGGGGGGGGG 19

RESULT 11
 US-10-289-660-205
 ; Sequence 205, Application US/10289660
 ; Publication No. US20030157561A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KOLKMAN, JOOST A.
 ; APPLICANT: STEMMER, WILLEM P.C.
 ; APPLICANT: GOVINDARAJAN, SRIDHAR
 ; TITLE OF INVENTION: COMBINATORIAL LIBRARIES OF MONOMER DOMAINS
 ; FILE REFERENCE: 0319.510US
 ; CURRENT APPLICATION NUMBER: US/10/289,660
 ; CURRENT FILING DATE: 2003-11-06
 ; PRIOR APPLICATION NUMBER: 10/133,128

PRIOR FILING DATE: 2002-04-26
PRIOR APPLICATION NUMBER: 60/374,107
PRIOR FILING DATE: 2002-04-18
PRIOR APPLICATION NUMBER: 60/333,359
PRIOR FILING DATE: 2001-11-26
PRIOR APPLICATION NUMBER: 60/337,209
PRIOR FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/286,823
PRIOR FILING DATE: 2001-04-26
NUMBER OF SEQ ID NOS: 244
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 205
LENGTH: 25
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: peptide linker
NAME/KEY: misc_feature
LOCATION: (1)..(12)
OTHER INFORMATION: This region may vary in length from 1-12 residues,
OTHER INFORMATION: 3-9 residues, 4-8 residues or 4-7 residues
FEATURE:
NAME/KEY: misc_feature
LOCATION: (14)..(25)
OTHER INFORMATION: This region may vary in length from 1-12 residues,
OTHER INFORMATION: 3-9 residues, 4-8 residues or 4-7 residues
US-10-289-660-205
Query Match 22.0%; Score 31; DB 14; Length 25;
Best Local Similarity 46.2%; Pred. No. 2.7e+03;
Matches 6; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 10 GKGDCACGDSGG 22
DB 7 GGGGGCGGGGG 19
RESULT 12
US-10-253-471-1099
Sequence 1099, Application US/10253471
Publication No. US20030236190A1
GENERAL INFORMATION:
APPLICANT: PILLUTLA, RENUKA et al.
TITLE OF INVENTION: INSULIN AND IGF-1 RECEPTOR AGONISTS AND ANTAGONISTS
FILE REFERENCE: 1878-4057
CURRENT APPLICATION NUMBER: US/10/253,471
PRIOR FILING DATE: 2002-09-24
PRIOR APPLICATION NUMBER: 09/962,756
PRIOR FILING DATE: 2001-09-24
PRIOR APPLICATION NUMBER: 09/538,038
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 09/146,127
NUMBER OF SEQ ID NOS: 227
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1099
LENGTH: 25
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: peptide
NAME/KEY: MOD RES
LOCATION: (13)
OTHER INFORMATION: Unknown amino acid; translation read-through at
OTHER INFORMATION: TGA stop codon
US-10-253-471-1099
Query Match 22.0%; Score 31; DB 15; Length 25;
Best Local Similarity 57.1%; Pred. No. 2.7e+03;
Matches 6; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 10 GKGDCACGDSGG 22
DB 7 GGGGGCGGGGG 19

MATCHES 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 18 GDSGGPF 24
DB 16 GEAGGPY 22
RESULT 13
US-10-253-493-1099
Sequence 1099, Application US/10253493
Publication No. US20040023887A1
GENERAL INFORMATION:
APPLICANT: PILLUTLA, RENUKA et al.
TITLE OF INVENTION: INSULIN AND IGF-1 RECEPTOR AGONISTS AND ANTAGONISTS
FILE REFERENCE: 1878-4056
CURRENT APPLICATION NUMBER: US/10/253,493
PRIOR FILING DATE: 2002-09-24
PRIOR APPLICATION NUMBER: 09/962,756
PRIOR FILING DATE: 2001-09-24
PRIOR APPLICATION NUMBER: 09/538,038
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 09/146,127
NUMBER OF SEQ ID NOS: 227
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1099
LENGTH: 25
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: peptide
NAME/KEY: MOD RES
LOCATION: (13)
OTHER INFORMATION: Unknown amino acid; translation read-through at
OTHER INFORMATION: TGA stop codon
US-10-253-493-1099
Query Match 22.0%; Score 31; DB 16; Length 25;
Best Local Similarity 57.1%; Pred. No. 2.7e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 18 GDSGGPF 24
DB 16 GEAGGPY 22
RESULT 14
US-09-933-767-598
Sequence 598, Application US/09933767
Publication No. US20030181692A1
GENERAL INFORMATION:
APPLICANT: Ni et al.
TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: P200722
CURRENT APPLICATION NUMBER: US/09/933,767
CURRENT FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: PCT/US01/05614
PRIOR FILING DATE: 2001-02-21
PRIOR APPLICATION NUMBER: 60/184,836
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: 60/193,170
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 09/205,258
PRIOR FILING DATE: 1998-12-04
PRIOR APPLICATION NUMBER: PCT/US98/11422
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/048,885
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/049,375
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,881

; PRIOR FILING DATE: 1997-06-06
 ; PRIOR APPLICATION NUMBER: 60/048,880
 ; PRIOR FILING DATE: 1997-06-06
 ; PRIOR APPLICATION NUMBER: 60/048,896
 ; PRIOR FILING DATE: 1997-06-06
 ; PRIOR APPLICATION NUMBER: 60/049,020
 ; PRIOR FILING DATE: 1997-06-06
 ; PRIOR APPLICATION NUMBER: 60/048,876
 ; PRIOR FILING DATE: 1997-06-06
 ; PRIOR APPLICATION NUMBER: 60/048,895
 ; PRIOR FILING DATE: 1997-06-06
 ; PRIOR APPLICATION NUMBER: 60/048,884
 ; PRIOR FILING DATE: 1997-06-06
 ; PRIOR APPLICATION NUMBER: 60/048,894
 ; PRIOR FILING DATE: 1997-06-06
 ; PRIOR APPLICATION NUMBER: 60/048,971
 ; PRIOR FILING DATE: 1997-06-06
 ; PRIOR APPLICATION NUMBER: 60/048,964
 ; PRIOR FILING DATE: 1997-06-06
 ; PRIOR APPLICATION NUMBER: 60/048,882
 ; PRIOR FILING DATE: 1997-06-06
 ; PRIOR APPLICATION NUMBER: 60/048,899
 ; PRIOR FILING DATE: 1997-06-06
 ; PRIOR APPLICATION NUMBER: 60/048,893
 ; PRIOR FILING DATE: 1997-06-06
 ; PRIOR APPLICATION NUMBER: 60/048,900
 ; PRIOR FILING DATE: 1997-06-06
 ; PRIOR APPLICATION NUMBER: 60/048,901
 ; PRIOR FILING DATE: 1997-06-06
 ; PRIOR APPLICATION NUMBER: 60/048,892
 ; PRIOR FILING DATE: 1997-06-06
 ; PRIOR APPLICATION NUMBER: 60/048,915
 ; PRIOR FILING DATE: 1997-06-06
 ; PRIOR APPLICATION NUMBER: 60/049,019
 ; PRIOR FILING DATE: 1997-06-06
 ; PRIOR APPLICATION NUMBER: 60/048,970
 ; PRIOR FILING DATE: 1997-06-06
 ; PRIOR APPLICATION NUMBER: 60/048,972
 ; PRIOR FILING DATE: 1997-06-06
 ; PRIOR APPLICATION NUMBER: 60/048,916
 ; PRIOR FILING DATE: 1997-06-06
 ; PRIOR APPLICATION NUMBER: 60/049,373
 ; PRIOR FILING DATE: 1997-06-06
 ; PRIOR APPLICATION NUMBER: 60/048,875
 ; PRIOR FILING DATE: 1997-06-06
 ; PRIOR APPLICATION NUMBER: 60/049,374
 ; PRIOR FILING DATE: 1997-06-06
 ; PRIOR APPLICATION NUMBER: 60/048,917
 ; PRIOR FILING DATE: 1997-06-06
 ; PRIOR APPLICATION NUMBER: 60/048,949
 ; PRIOR FILING DATE: 1997-06-06
 ; PRIOR APPLICATION NUMBER: 60/048,974
 ; PRIOR FILING DATE: 1997-06-06
 ; PRIOR APPLICATION NUMBER: 60/048,883
 ; PRIOR FILING DATE: 1997-06-06
 ; PRIOR APPLICATION NUMBER: 60/048,897
 ; PRIOR FILING DATE: 1997-06-06
 ; PRIOR APPLICATION NUMBER: 60/048,898
 ; PRIOR FILING DATE: 1997-06-06
 ; PRIOR APPLICATION NUMBER: 60/048,962
 ; PRIOR FILING DATE: 1997-06-06
 ; PRIOR APPLICATION NUMBER: 60/048,963
 ; PRIOR FILING DATE: 1997-06-06
 ; PRIOR APPLICATION NUMBER: 60/048,877
 ; PRIOR FILING DATE: 1997-06-06
 ; PRIOR APPLICATION NUMBER: 60/048,878
 ; PRIOR FILING DATE: 1997-06-06
 ; PRIOR APPLICATION NUMBER: 60/068,054
 ; PRIOR FILING DATE: 1997-12-18
 ; PRIOR APPLICATION NUMBER: 60/068,064
 ; PRIOR FILING DATE: 1997-12-18
 ; PRIOR APPLICATION NUMBER: 60/068,053
 ; PRIOR FILING DATE: 1997-12-18

; PRIOR APPLICATION NUMBER: 60/070,923
 ; PRIOR FILING DATE: 1997-12-18
 ; PRIOR APPLICATION NUMBER: 60/073,160
 ; PRIOR FILING DATE: 1998-01-30
 ; PRIOR APPLICATION NUMBER: 60/073,159
 ; PRIOR FILING DATE: 1998-01-30
 ; PRIOR APPLICATION NUMBER: 60/073,165
 ; PRIOR FILING DATE: 1998-01-30
 ; PRIOR APPLICATION NUMBER: 60/073,164
 ; PRIOR FILING DATE: 1998-01-30
 ; PRIOR APPLICATION NUMBER: 60/085,925
 ; PRIOR FILING DATE: 1998-05-18
 ; PRIOR APPLICATION NUMBER: 60/085,921
 ; PRIOR FILING DATE: 1998-05-18
 ; PRIOR APPLICATION NUMBER: 60/085,923
 ; PRIOR FILING DATE: 1998-05-18
 ; PRIOR APPLICATION NUMBER: 60/085,922
 ; PRIOR FILING DATE: 1998-05-18
 ; PRIOR APPLICATION NUMBER: 60/092,921
 ; PRIOR FILING DATE: 1998-07-15
 ; PRIOR APPLICATION NUMBER: 60/094,857
 ; PRIOR FILING DATE: 1998-07-30
 ; NUMBER OF SEQ ID NOS: 1245
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 598
 ; LENGTH: 25
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-933-767-598

 Query Match 21.3%; Score 30; DB 10; Length 25;
 Best Local Similarity 42.9%; Pred. No. 3.7e+03;
 Matches 6; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

 QY 9 EGKRGDACEGDSGG 22
 DB 4 EGKRRACKNCTCG 17

 RESULT 15
 US-10-036-869-7
 ; Sequence 7, Application US/10036869
 ; Publication No. US20020151516A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Mixson, James A
 ; TITLE OF INVENTION: CARRIER:DNA COMPLEXES CONTAINING DNA
 ; THERAPY
 ; NUMBER OF SEQUENCES: 43
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Connolly, Bove, Lodge, & Hutz
 ; STREET: 1220 Market Street, P.O. Box 2207
 ; CITY: Wilmington
 ; STATE: Delaware
 ; COUNTRY: U.S.A.
 ; ZIP: 19899
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/036,869
 ; FILING DATE: 29-Nov. US20020151516A1-2001
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/985,526
 ; FILING DATE: <Unknown>
 ; APPLICATION NUMBER: US 08/608,845
 ; FILING DATE: 16-JUL-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: McMorrow Jr., Robert G
 ; TELECOMMUNICATION INFORMATION:

Mon Mar 22 14:25:14 2004

```

;
; TELEPHONE: (302) 658-9141
; TELEFAX: (302) 658-5613
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-036-859-7

Query Match      21.3%; Score 30; DB 13; Length 25;
Best Local Similarity 40.0%; Pred. No. 3.7e+03;
Matches 8; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

QY      2 GTRYKPDGKRGDACEGDSG 21
      |.:|:|:|:|:|:|:|:|:|
DB      4 GSRGKSYIGSRGKSYIGSRG 23

Search completed: March 18, 2004, 07:28:45
Job time : 40 secs

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; Patent No. US20020128202A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; APPLICANT: Crowther, Roger S.
; APPLICANT: Simmons, David J.
; APPLICANT: Yang, Jinping
; APPLICANT: Redin, William R.
; TITLE OF INVENTION: Stimulation Of Bone Growth With Thrombin
; TITLE OF INVENTION: Peptide Derivatives
; FILE REFERENCE: 3033.1002-001
; CURRENT APPLICATION NUMBER: US/09/909,122
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/219,300
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide fragment of Thrombin
US-09-909-122-5

Query Match 100.0%; Score 141; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 6.2e-12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTRYKPDGKRGDACEGDSGGPFV 25
| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 AGTRYKPDGKRGDACEGDSGGPFV 25

RESULT 3
US-10-050-692-5
; Sequence 5, Application US/10050692
; Publication No. US2002018205A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; APPLICANT: Crowther, Roger S.
; APPLICANT: Simmons, David J.
; APPLICANT: Yang, Jinping
; APPLICANT: Redin, William R.
; TITLE OF INVENTION: STIMULATION OF BONE GROWTH WITH THROMBIN
; TITLE OF INVENTION: PEPTIDE DERIVATIVES
; FILE REFERENCE: 3033.1002-004
; CURRENT APPLICATION NUMBER: US/10/050,692
; CURRENT FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: 09/909,122
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/219,300
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fragment of human prothrombin
US-10-050-692-5

Query Match 100.0%; Score 141; DB 13; Length 25;
Best Local Similarity 100.0%; Pred. No. 6.2e-12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTRYKPDGKRGDACEGDSGGPFV 25
| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 AGTRYKPDGKRGDACEGDSGGPFV 25

RESULT 4
US-09-777-328-8

; Sequence 8, Application US/09777328
; Patent No. US20020032314A1
; GENERAL INFORMATION:
; APPLICANT: CARNEY, DARRELL H.
; APPLICANT: RAMAKRISHNAN, SHYAM
; TITLE OF INVENTION: SYNTHETIC PEPTIDE NEUTROPHIL CELL CHEMOTRACTIC AGENTS
; FILE REFERENCE: CHBP:002
; CURRENT APPLICATION NUMBER: US/09/777,328
; CURRENT FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 08/330,594
; PRIOR FILING DATE: 1994-10-28
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 8
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-777-328-8

Query Match 85.8%; Score 121; DB 9; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.6e-09;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 YKPDEGKRGDACEGDSGGPFV 25
| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 3 YKPDEGKRGDACEGDSGGPFV 23

RESULT 5
US-09-904-090-3
; Sequence 3, Application US/09904090
; Patent No. US20020061852A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell
; TITLE OF INVENTION: METHODS OF THERAPY WITH THROMBIN DERIVED
; FILE REFERENCE: 3033.1000-001
; CURRENT APPLICATION NUMBER: US/09/904,090
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: US 60/217,583
; PRIOR FILING DATE: 2000-07-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide, fragment of thrombin
US-09-904-090-3

Query Match 85.8%; Score 121; DB 9; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.6e-09;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 YKPDEGKRGDACEGDSGGPFV 25
| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 3 YKPDEGKRGDACEGDSGGPFV 23

RESULT 6
US-10-050-611-3
; Sequence 3, Application US/10050611
; Publication No. US20020187933A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; TITLE OF INVENTION: METHODS OF THERAPY WITH THROMBIN DERIVED
; TITLE OF INVENTION: PEPTIDES
; FILE REFERENCE: 3033.1000-008
; CURRENT APPLICATION NUMBER: US/10/050,611
US-10-050-611-3

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; CURRENT FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: 09/904,090
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 60/217,583
; PRIOR FILING DATE: 2000-07-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human fragment of thrombin
US-10-050-611-3

Query Match      85.8%; Score 121; DB 13; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.6e-09;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 YKPDEGKRGDACEGDSGGPFV 25
   |||||
Db 3 YKPDEGKRGDACEGDSGGPFV 23

RESULT 7
US-10-050-611-4
; Sequence 4, Application US/10050611
; Publication No. US20020187933A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; TITLE OF INVENTION: METHODS OF THERAPY WITH THROMBIN DERIVED
; TITLE OF INVENTION: PEPTIDES
; FILE REFERENCE: 3033.1000-008
; CURRENT APPLICATION NUMBER: US/10/050,611
; PRIOR FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: 09/904,090
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 60/217,583
; PRIOR FILING DATE: 2000-07-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: c-terminal amidated fragment of human thrombin
; NAME/KEY: AMIDATION
; LOCATION: 23
; OTHER INFORMATION: valine is amidated as CONH2
US-10-050-611-4

Query Match      85.8%; Score 121; DB 13; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.6e-09;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 YKPDEGKRGDACEGDSGGPFV 25
   |||||
Db 3 YKPDEGKRGDACEGDSGGPFV 23

RESULT 8
US-10-050-688-5
; Sequence 5, Application US/10050688
; Publication No. US20020198154A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; APPLICANT: Crowther, Roger S.
; APPLICANT: Stierberg, Janet
; APPLICANT: Bergmann, John
; TITLE OF INVENTION: STIMULATION OF CARTILAGE GROWTH WITH
; TITLE OF INVENTION: AGONISTS OF THE NON-PROTEOLYTICALLY ACTIVATED THROMBIN
```

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; TITLE OF INVENTION: RECEPTOR
; FILE REFERENCE: 3033.1003-004
; CURRENT APPLICATION NUMBER: US/10/050,688
; CURRENT FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: 09/909,348
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/219,800
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide fragment of thrombin
US-10-050-688-5

Query Match      85.8%; Score 121; DB 13; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.6e-09;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 YKPDEGKRGDACEGDSGGPFV 25
   |||||
Db 3 YKPDEGKRGDACEGDSGGPFV 23

RESULT 9
US-10-050-688-6
; Sequence 6, Application US/10050688
; Publication No. US20020198154A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; APPLICANT: Crowther, Roger S.
; APPLICANT: Stierberg, Janet
; APPLICANT: Bergmann, John
; TITLE OF INVENTION: STIMULATION OF CARTILAGE GROWTH WITH
; TITLE OF INVENTION: AGONISTS OF THE NON-PROTEOLYTICALLY ACTIVATED THROMBIN
; FILE REFERENCE: 3033.1003-004
; CURRENT APPLICATION NUMBER: US/10/050,688
; CURRENT FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: 09/909,348
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/219,800
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide fragment of thrombin
; NAME/KEY: AMIDATION
; LOCATION: (23)...(23)
; OTHER INFORMATION: CONH2
US-10-050-688-6

Query Match      85.8%; Score 121; DB 13; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.6e-09;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 YKPDEGKRGDACEGDSGGPFV 25
   |||||
Db 3 YKPDEGKRGDACEGDSGGPFV 23

RESULT 10
US-10-165-442-2
; Sequence 2, Application US/10165442
; Publication No. US20030215440A1
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; GENERAL INFORMATION:
; APPLICANT: Emory University
; TITLE OF INVENTION: Antithrombotic Variant Thrombins
; FILE REFERENCE: E056 1070.1
; CURRENT APPLICATION NUMBER: US/10/165,442
; CURRENT FILING DATE: 2002-06-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 259
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: CHAIN
; LOCATION: (1)..(259)
; OTHER INFORMATION: Thrombin W215A B-Chain
US-10-165-442-2

Query Match      85.8%; Score 121; DB 15; Length 259;
Best Local Similarity 100.0%; Pred. No. 3.2e-08;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 YKPDEGKRGDACEGDSGGPFV 25
Db      190 YKPDEGKRGDACEGDSGGPFV 210

RESULT 11
US-10-165-442-4
; Sequence 4, Application US/10165442
; Publication No. US20030215440A1
; GENERAL INFORMATION:
; APPLICANT: Emory University
; TITLE OF INVENTION: Antithrombotic Variant Thrombins
; FILE REFERENCE: E056 1070.1
; CURRENT APPLICATION NUMBER: US/10/165,442
; CURRENT FILING DATE: 2002-06-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 259
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: CHAIN
; LOCATION: (1)..(259)
; OTHER INFORMATION: Thrombin WE B-Chain
US-10-165-442-4

Query Match      85.8%; Score 121; DB 15; Length 259;
Best Local Similarity 100.0%; Pred. No. 3.2e-08;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 YKPDEGKRGDACEGDSGGPFV 25
Db      190 YKPDEGKRGDACEGDSGGPFV 210

RESULT 12
US-10-165-442-1
; Sequence 1, Application US/10165442
; Publication No. US20030215440A1
; GENERAL INFORMATION:
; APPLICANT: Emory University
; TITLE OF INVENTION: Antithrombotic Variant Thrombins
; FILE REFERENCE: E056 1070.1
; CURRENT APPLICATION NUMBER: US/10/165,442
; CURRENT FILING DATE: 2002-06-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 295
; TYPE: PRT
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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; LOCATION: (1)..(36)
; OTHER INFORMATION: Thrombin W215A A-Chain
; FEATURE:
; NAME/KEY: CHAIN
; LOCATION: (37)..(295)
; OTHER INFORMATION: Thrombin W215A B-Chain
US-10-165-442-1

Query Match      85.8%; Score 121; DB 15; Length 295;
Best Local Similarity 100.0%; Pred. No. 3.6e-08;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 YKPDEGKRGDACEGDSGGPFV 25
Db      226 YKPDEGKRGDACEGDSGGPFV 246

RESULT 13
US-10-165-442-3
; Sequence 3, Application US/10165442
; Publication No. US20030215440A1
; GENERAL INFORMATION:
; APPLICANT: Emory University
; TITLE OF INVENTION: Antithrombotic Variant Thrombins
; FILE REFERENCE: E056 1070.1
; CURRENT APPLICATION NUMBER: US/10/165,442
; CURRENT FILING DATE: 2002-06-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 295
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; LOCATION: (1)..(36)
; OTHER INFORMATION: Thrombin WE A-Chain
; FEATURE:
; NAME/KEY: CHAIN
; LOCATION: (37)..(295)
; OTHER INFORMATION: Thrombin WE B-Chain
US-10-165-442-3

Query Match      85.8%; Score 121; DB 15; Length 295;
Best Local Similarity 100.0%; Pred. No. 3.6e-08;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 YKPDEGKRGDACEGDSGGPFV 25
Db      226 YKPDEGKRGDACEGDSGGPFV 246

RESULT 14
US-10-020-141-8
; Sequence 8, Application US/10020141
; Publication No. US2003092013A1
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Jeanette
; APPLICANT: Ableson, Allen
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF VASCULAR DISEASE
; FILE REFERENCE: MMI-002
; CURRENT APPLICATION NUMBER: US/10/020,141
; CURRENT FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/313,097
; PRIOR FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: US 60/327,485
; PRIOR FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
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; LENGTH: 622
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-020-141-8

Query Match      85.8%; Score 121; DB 14; Length 622;
Best Local Similarity 100.0%; Pred. No. 7.8e-08;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 YKPDGKRGDACEGDSGGPFV 25
Db      553 YKPDGKRGDACEGDSGGPFV 573

RESULT 15
US-10-017-631-2
; Sequence 2, Application US/10017631
; Publication No. US2003009957A1
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Jeanette
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF VASCULAR DISEASE
; FILE REFERENCE: WMI-006
; CURRENT APPLICATION NUMBER: US/10/017,631
; CURRENT FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: 60/325,930
; PRIOR FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 622
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-017-631-2

Query Match      85.8%; Score 121; DB 14; Length 622;
Best Local Similarity 100.0%; Pred. No. 7.8e-08;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 YKPDGKRGDACEGDSGGPFV 25
Db      553 YKPDGKRGDACEGDSGGPFV 573
```

Search completed: March 18, 2004, 07:24:53
Job time : 66.4762 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 26, 2004, 09:17:19 ; Search time 13.5 Seconds
(without alignments)
71.253 Million cell updates/sec

Title: US-09-909-348-1

Perfect score: 59

Sequence: 1 CEGDSGGPFV 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 311

Minimum DB seq length: 10

Maximum DB seq length: 10

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 78:*

1: piri:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	23	39.0	10	2 XGHUE	erythrocyte membra
2	20	33.9	10	2 PH0927	T-cell receptor be
3	20	33.9	10	2 PH0925	T-cell receptor be
4	19	32.2	10	2 PH0944	T-cell receptor be
5	18	30.5	10	2 C39572	sperm-activating p
6	18	30.5	10	2 B60589	sperm-activating p
7	17	28.8	10	2 B49581	sialokinin II - ye
8	17	28.8	10	2 C61440	polygalacturonase
9	17	28.8	10	2 PH1344	Ig heavy chain DJ
10	17	28.8	10	2 PT0632	T-cell receptor be
11	17	28.8	10	2 PT0664	T-cell receptor be
12	16	27.1	10	2 D60787	sperm-activating p
13	16	27.1	10	2 D60527	sperm-activating p
14	16	27.1	10	2 E39572	sperm-activating p
15	16	27.1	10	2 F60589	sperm-activating p
16	16	27.1	10	2 D60589	sperm-activating p
17	16	27.1	10	2 E60589	sperm-activating p
18	16	27.1	10	2 A60588	sperm-activating p
19	16	27.1	10	2 AN0165	triose-phosphate i
20	16	27.1	10	2 A24196	acetylcholinestera
21	16	27.1	10	2 PT0243	Ig heavy chain CRD
22	16	27.1	10	2 PT0215	T-cell receptor be
23	16	27.1	10	2 B41946	T-cell receptor ga
24	16	27.1	10	2 PH0900	T-cell receptor be
25	16	27.1	10	2 S68033	cytochrome P450 1A
26	15	25.4	10	1 ECLQ1M	tachykinin I - mig
27	15	25.4	10	2 S23171	T-cell receptor al
28	14	23.7	10	1 XASNPC	angiotensin-conver
29	14	23.7	10	2 S39374	mannose receptor -

30	14	23.7	10	2 F60527	sperm-activating p
31	14	23.7	10	2 S48182	bacterioferritin -
32	14	23.7	10	2 P10084	protein O8600021 -
33	14	23.7	10	2 D28027	protein P7 - curle
34	14	23.7	10	2 PX0060	lysosome-associate
35	14	23.7	10	2 A32195	Na+/K+-exchanging
36	13	22.0	10	2 S65388	cytochrome-c oxida
37	13	22.0	10	2 A60624	angiotensin I - Ja
38	13	22.0	10	2 C45474	thrombospondin 2 -
39	13	22.0	10	2 B33710	ornithine decarbox
40	13	22.0	10	2 H60787	sperm-activating p
41	13	22.0	10	2 C60788	sperm-activating p
42	13	22.0	10	2 D60788	sperm-activating p
43	13	22.0	10	2 C60787	sperm-activating p
44	13	22.0	10	2 A60787	sperm-activating p
45	13	22.0	10	2 B60787	sperm-activating p

ALIGNMENTS

RESULT 1

XGHUE

erythrocyte membrane glycopeptide - human

C:Species: Homo sapiens (man)

C>Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000

C:Accession: A03187

R:Weiss, J.B.; Lote, C.J.; Bobinski, H.

Nature New Biol. 234, 25-26, 1971

A:Title: New low molecular weight glycopeptide containing triglycosylcysteine in human e

A:Reference number: A03187; MUID:72034940; PMID:5286858

A:Accession: A03187

A:Molecule type: protein

A:Residues: 1-10 <WEI>

C:Comment: The identity of the glycoprotein from which this peptide is derived is unknown

found (see PIR:XGHUEU).

C:Superfamily: unassigned animal peptides

C:Keywords: glycoprotein

F:Binding site: carbohydrate (Cys) (covalent) #status experimental

Query Match 39.0%; Score 23; DB 2; Length 10;

Best Local Similarity 80.0%; Pred. No. 6.8e+02;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CEGDS 5

DB 1 CEGHS 5

RESULT 2

PH0927

T-cell receptor beta chain V-D-J region (clone 13) - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)

C>Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997

C:Accession: PH0927

R:Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.

J. Exp. Med. 174, 1467-1476, 1991

A:Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergi

A:Reference number: PH0891; MUID:92078857; PMID:1836012

A:Accession: PH0927

A:Molecule type: mRNA

A:Residues: 1-10 <GOL>

A:Experimental source: concanavalin A-activated lymphoblast

C:Keywords: T-cell receptor

Query Match 33.9%; Score 20; DB 2; Length 10;

Best Local Similarity 60.0%; Pred. No. 2.2e+03;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 SGGPF 9

DB 4 SAGPY 8

Query Match 28.8%; Score 17; DB 2; Length 10;
 Best Local Similarity 75.0%; Pred. No. 7.2e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 6 GGPF 9
 ||||
 Db 2 GGAF 5

RESULT 9

PH1344
 Ig heavy chain DJ region (clone C100-91A) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
 C:Accession: PH1344
 R:Wasserman, R.; Galli, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
 J. Exp. Med. 176, 1577-1581, 1992
 A:Title: Predominance of fetal type DJH joining in young children with B precursor lymphoma
 A:Reference number: PH1302; MUID:93094761; PMID:1450419
 A:Accession: PH1344
 A:Molecule type: DNA
 A:Residues: 1-10 <WAS>
 C:Keywords: heterotetramer; immunoglobulin

Query Match 28.8%; Score 17; DB 2; Length 10;
 Best Local Similarity 60.0%; Pred. No. 7.2e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 BGDSS 6

|||

Db 3 DGDWG 7

RESULT 10

PT0632
 T-cell receptor beta chain V-D-J region (120-1A) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C:Accession: PT0632
 R:Feeney, A.J.
 J. Exp. Med. 174, 115-124, 1991

A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
 A:Reference number: PT0509; MUID:91277601; PMID:1711558
 A:Accession: PT0632
 A>Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-10 <FEE>
 A:Experimental source: newborn thymus, strain BALB/c
 C:Keywords: T-cell receptor

Query Match 28.8%; Score 17; DB 2; Length 10;
 Best Local Similarity 60.0%; Pred. No. 7.2e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 GDSGG 7

|||

Db 3 GDAPG 7

RESULT 11

PT0664
 T-cell receptor beta chain V-D-J region (121-2L) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C:Accession: PT0664
 R:Feeney, A.J.
 J. Exp. Med. 174, 115-124, 1991

A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
 A:Reference number: PT0509; MUID:91277601; PMID:1711558
 A:Accession: PT0664
 A>Status: translation not shown
 A:Molecule type: mRNA

A:Residues: 1-10 <FEE>
 A:Experimental source: day 4 postnatal thymus, strain BALB/c
 C:Keywords: T-cell receptor

Query Match 28.8%; Score 17; DB 2; Length 10;
 Best Local Similarity 60.0%; Pred. No. 7.2e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 GDSGG 7

|||

Db 3 GDTPG 7

RESULT 12

F60787
 sperm-activating peptide (Ser-5 speract) - sea urchin (Anthocidaris crassispina)
 C:Species: Anthocidaris crassispina
 C:Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 18-Aug-2000
 C:Accession: F60787
 R:Suzuki, N.; Kajiyura, H.; Nomura, K.; Garbers, D.L.; Yoshino, K.; Kurita, M.; Tanaka, H.
 Comp. Biochem. Physiol. B 89, 687-693, 1988
 A:Title: Some more speract derivatives associated with eggs of sea urchins, Pseudocentrotus
 A:Reference number: A60787; MUID:88242184; PMID:3378407
 A:Accession: F60787
 A:Molecule type: protein
 A:Residues: 1-10 <SUZ>
 C:Comment: This oligopeptide from egg jelly is one of several from this species, all of which
 at shows some, but not absolute, species restriction.
 C:Superfamily: unassigned animal peptides

Query Match 27.1%; Score 16; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 SGG 7

|||

Db 5 SGG 7

RESULT 13

D60527
 sperm-activating peptide (Gly-5 SAP-I) - sea urchin (Tripneustes gratilla)
 N:Alternate names: speract homolog TG-6
 C:Species: Tripneustes gratilla
 C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Aug-2000
 C:Accession: D60527; F39572
 R:Yoshino, K.I.; Kajiyura, H.; Nomura, K.; Takao, T.; Shimonishi, Y.; Kurita, M.; Yamaguchi,
 Comp. Biochem. Physiol. B 94, 739-751, 1989
 A:Title: A halogenated amino acid-containing sperm activating peptide and its related peptide
 otus nudus, Echinometra mathaei and Heterocentrotus mamillatus.
 A:Reference number: A60527
 A:Accession: D60527

A:Molecule type: protein
 A:Residues: 1-10 <YOS>
 A:Note: this peptide did not contain bromophenylalanine
 R:Yoshino, K.; Takao, T.; Sunara, M.; Kitai, T.; Hori, H.; Nomura, K.; Yamaguchi, M.; Sh.
 Biochemistry 30, 6203-6209, 1991
 A:Title: Identification of a novel amino acid, o-bromo-L-phenylalanine, in egg-associated
 A:Reference number: A39572; MUID:91283461; PMID:2059627
 A:Accession: F39572
 A:Molecule type: protein
 A:Residues: 1-10 <YOS>

A:Note: this peptide contained bromophenylalanine
 C:Superfamily: unassigned animal peptides
 C:Keywords: bromine
 F;2/Modified site: 2'-bromophenylalanine (Phe) (partial) #status experimental

Query Match 27.1%; Score 16; DB 2; Length 10;
 Best Local Similarity 75.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 DSGG 7

|||

```

Db          3 DLGG 6

RESULT 14
E39572
sperm-activating peptide TG-5 - sea urchin (Tripneustes gratilla)
N:Alternate names: speract homolog TG-5
C:Species: Tripneustes gratilla
C>Date: 10-Jul-1992 #sequence_revision 10-Jul-1992 #text_change 18-Aug-2000
C:Accession: E39572
R:Yoshino, K.; Takao, T.; Suhara, M.; Kitai, T.; Hori, H.; Nomura, K.; Yamaguchi, M.; Sh
Biochemistry 30, 6203-6209, 1991
A:Title: Identification of a novel amino acid, o-bromo-L-phenylalanine, in egg-associated
A:Reference number: A39572; PMID:91283461; PMID:2059627
A:Accession: E39572
A:Molecule type: protein
A:Residues: 1-10 <YOS>
C:Superfamily: unassigned animal peptides
C:Keywords: bromine
F:2/Modified site: 2'-bromophenylalanine (Phe) #status experimental

Query Match          27.1%; Score 16; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          5 SGG 7
           |||
Db          5 SGG 7

RESULT 15
F60589
sperm-activating peptide (Asn-3, Ser-5 SAP-I) - Echinometra mathaei (type A)
C:Species: Echinometra mathaei
C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Aug-2000
C:Accession: F60589
R:Yoshino, K.I.; Kajiwara, H.; Nomura, K.; Takao, T.; Shimonishi, Y.; Kurita, M.; Yamaguc
Comp. Biochem. Physiol. B 94, 739-751, 1989
A:Title: A halogenated amino acid-containing sperm activating peptide and its related pe
otus nudus, Echinometra mathaei and Heterocentrotus mamillatus.
A:Reference number: A60527
A:Accession: F60589
A:Molecule type: protein
A:Residues: 1-10 <YOS>
C:Superfamily: unassigned animal peptides

Query Match          27.1%; Score 16; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          5 SGG 7
           |||
Db          5 SGG 7

Search completed: February 26, 2004, 09:24:05
Job time : 14.5 secs

```

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OM protein - protein search, using sw model

Run on: February 26, 2004, 09:02:09 : Search time 10.5 Seconds
(without alignments)
49.591 Million cell updates/sec

Title: US-09-909-348-1
Perfect score: 59
Sequence: 1 CEGDSGGPFV 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues
Total number of hits satisfying chosen parameters: 120

Minimum DB seq length: 10
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	23	39.0	10	1 GLEM_HUMAN	P02728 homo sapien
2	17	28.8	10	1 FAR6_PANRE	P82660 panagrellus
3	17	28.8	10	1 TK52_AEDAE	P42635 aedes aegypt
4	16	27.1	10	1 ESTA_SCHGA	P81012 schizaphis
5	15	25.4	10	1 COXQ_PABIT	P80336 erythrocyte
6	14	23.7	10	1 BPF_VIPAS	P31351 vipera aspi
7	14	23.7	10	1 RCA_PINPS	P81084 pinus pinas
8	13	22.0	10	1 ANGI_BOTJA	Q10581 bothrops ja
9	13	22.0	10	1 ANGT_BOVIN	P01017 bos taurus
10	13	22.0	10	1 ANGT_CHICK	P01018 gallus gall
11	13	22.0	10	1 COXO_RAT	P80432 rattus norv
12	13	22.0	10	1 COXO_THIOB	P80982 thunnus obe
13	13	22.0	10	1 PNEU_HUMAN	P22103 homo sapien
14	13	22.0	10	1 PNEU_RAT	P21996 rattus norv
15	13	22.0	10	1 RT02_BOVIN	P82923 bos taurus
16	13	22.0	10	1 TRP8_LEUMA	P81740 leucophaea
17	12	20.3	10	1 COXH_ONCMY	P80331 oncorhynch
18	12	20.3	10	1 CU30_LOCOM	P11735 locusta mig
19	12	20.3	10	1 FAR7_NACRS	P83280 macrobrachi
20	12	20.3	10	1 FARP_MYTED	P43560 mytilus edu
21	12	20.3	10	1 MOSQ_CLIYA	P19662 clypeaster
22	12	20.3	10	1 TK51_AEDAE	P42634 aedes aegypt
23	12	20.3	10	1 TPIS_NICPL	P19118 nicotiana p
24	11	18.6	10	1 AMEN_HELAM	P81731 helicoverpa
25	11	18.6	10	1 LSK2_LEUMA	P09039 leucophaea
26	11	18.6	10	1 NS1_MYCTU	P81135 mycobacteri
27	11	18.6	10	1 PPKX_FASHE	P80525 fasciola he
28	11	18.6	10	1 TKNB_RANCA	P22689 rana catesb
29	10	16.9	10	1 CA12_LITCI	P82086 litorea cit
30	10	16.9	10	1 CATS_SHEEP	P83205 ovis aries
31	10	16.9	10	1 GAJU_SHEEP	P01358 homo.sapien
32	10	16.9	10	1 GONI_CLUPA	P81749 clupea pall
33	10	16.9	10	1 HTF_HELIZE	P16353 heliothis z

34	10	16.9	10	1 PVK_LOCOM	P83382 locusta mig
35	10	16.9	10	1 RPL_PHODV	P35946 phocine dis
36	10	16.9	10	1 SPI_HALSO	Q10997 halocynthia
37	10	16.9	10	1 TKLZ_LOCOM	P16224 locusta mig
38	10	16.9	10	1 TKNB_CHICK	P19851 gallus gall
39	10	16.9	10	1 TKNB_ONCMY	P28500 oncorhynch
40	10	16.9	10	1 TKNB_RANRI	P29135 rana ridibu
41	10	16.9	10	1 TKNK_PIG	P01292 sus scrofa
42	10	16.9	10	1 TKU1_UREUN	P40751 urechis uni
43	10	16.9	10	1 TMOF_AEDAE	P19425 aedes aegyp
44	10	16.9	10	1 TRP7_LEUMA	P81739 leucophaea
45	10	16.9	10	1 UH05_RAT	P56573 rattus norv

ALIGNMENTS

```
RESULT 1
ID GLEM_HUMAN STANDARD; PRT; 10 AA.
AC P02728;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Erythrocyte membrane glycopeptide.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=72034940; PubMed=5286858;
RA Weiss J.B., Lote C.J., Bobinski H.;
RT "New low molecular weight glycopeptide containing triglucoylcysteine
RL in human erythrocyte membrane."
RL Nature New Biol. 234:25-26(1971).
CC -!- PTM: S-linked glycan consists of GLC-GLC-Glc trisaccharide.
CC -!- MISCELLANEOUS: The identity of the glycoprotein from which this
CC peptide is derived is unknown. No physiological function has been
CC attributed.
DR PIR; A03187; XGHUE.
KW Glycoprotein; Erythrocyte.
FT CARBOHYD 1
SQ SEQUENCE 10 AA; 1049 MW; 239BFEEA1F5B1E8 CRC64;
Query Match 39.0%; Score 23; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 2e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 1;

Qy 1 CEGDS 5
Db 1 CEGHS 5

RESULT 2
ID FAR6_PANRE STANDARD; PRT; 10 AA.
AC P82660;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE FMRamide-like neuropeptide PF6 (NGAPQPFVRF-amide).
OS Panagrellus redivivus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
OC Panagrolaimoidea; Panagrolaimidae; Panagrellus.
OX NCBI_TaxID=6233;
RN [1]
RP SEQUENCE, FUNCTION, AND AMIDATION.
RA Moffett C.L., Marks N.J., Halton D.W., Thomson D.P., Geary T.G.,
RA Maule A.G.;
RT "Isolation, characterization and pharmacology of FMRamide-related
RT peptides (FARPs) from free-living nematode, Panagrellus redivivus.";
RT Submitted (JUL-2000) to Swiss-Prot.
```

```
CC -!- FUNCTION: Myoactive.
CC -!- SIMILARITY: Belongs to the FARP (FMRPamide related peptide)
CC family.
KW Neuropeptide; Amidation.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1132 MW; CB13E4C9D776C76D CRC64;

Query Match 28.8%; Score 17; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PFV 10
DB 6 PFV 8

RESULT 3
TKS2_AEDAE
ID_TKS2_AEDAE STANDARD; PRT; 10 AA.
AC P42635;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Sialokinin II.
OS Aedes aegypti (Yellowfever mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.
OX NCBI_TaxID=7159;
RN [1]_
SEQUENCE.
RP STRAIN=Rockefeller; TISSUE=Salivary gland;
RX MEDLINE=94105119; PubMed=8278354;
RA Champagne D.E., Ribeiro J.M.C.;
RT "Sialokinin I and II: vasodilatory tachykinins from the yellow fever
RT mosquito Aedes aegypti.",
RL Proc. Natl. Acad. Sci. U.S.A. 91:138-142(1994).
CC -!- FUNCTION: Vasodilatory peptide. May activate macrophages at the
CC site of feeding.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the tachykinin family.
DR PIR; B49581;
DR InterPro; IPR002040; Tachy Neurokinin.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1146 MW; 3DC77C6B59C33AA8 CRC64;

Query Match 28.8%; Score 17; DB 1; Length 10;
Best Local Similarity 50.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 DSGGPF 9
DB 1 DTGDKF 6

RESULT 4
ESTA_SCHGA
ID_ESTA_SCHGA STANDARD; PRT; 10 AA.
AC P81012;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Esterase 52 kDa subunit (EC 3.1.1.1) (Carboxylic-ester hydrolase)
DE (Fragment).
OS Schizaphis graminum (Aphid).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
OC Aphidoidea; Aphididae; Aphidini; Schizaphis.
OX NCBI_TaxID=13262;
RN [1]_
SEQUENCE.
RP MEDLINE=97468499; PubMed=9327586;

RA Siegfried B.D., Ono M., Swanson J.J.;
RT "Purification and characterization of a carboxylesterase associated
RT with organophosphate resistance in the greenbug, Schizaphis graminum
RT (Homoptera: Aphididae).";
RL Arch. Insect Biochem. Physiol. 36:229-240(1997).
CC -!- CATALYTIC ACTIVITY: A carboxylic ester + H(2)O = an alcohol + a
CC carboxylic anion.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC InterPro; IPR002018; Carboxylesterase.
DR PROSITE; PS00222; CARBOXYLESTERASE_B_1; PARTIAL.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; PARTIAL.
KW Hydrolase; Serine esterase.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1025 MW; 018ABE587865A2C0 CRC64;

Query Match 27.1%; Score 16; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 SGG 7
DB 5 SGG 7

RESULT 5
COXQ_RABIT
ID_COXQ_RABIT STANDARD; PRT; 10 AA.
AC P80336;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytochrome c oxidase polypeptide VIII-liver/heart (EC 1.9.3.1)
DE (Fragment).
GN COX8H.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]_
SEQUENCE.
RP TISSUE=Heart, and Liver;
RC Freund R., Kadenbach B.;
RA Submitted (MAR-1994) to Swiss-Prot.
RL -!- FUNCTION: This protein is one of the nuclear-coded polypeptide
RL chains of cytochrome c oxidase, the terminal oxidase in
RL mitochondrial electron transport.
CC -!- CATALYTIC ACTIVITY: 4 ferrocytchrome c + O(2) = 4 ferricytochrome
CC c + 2 H(2)O.
CC -!- SIMILARITY: Belongs to the cytochrome c oxidase VIII family.
CC Oxidoreductase; Mitochondrion.
KW NON_TER 10 10
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1027 MW; 2C325CB40DC76338 CRC64;

Query Match 25.4%; Score 15; DB 1; Length 10;
Best Local Similarity 75.0%; Pred. No. 5.3e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 SGGP 8
DB 2 SGKP 5

RESULT 6
BPP_VIPAS
ID_BPP_VIPAS STANDARD; PRT; 10 AA.
AC P31351;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide (Angiotensin-converting
DE enzyme inhibitor).
OS Vipera aspis (Aspic viper).
```

CC physiologically active peptide angiotensin II, the most potent
CC pressor substance known, which helps regulate volume and mineral
CC balance of body fluids.
CC
CC -! SUBCELLULAR LOCATION: Secreted.
CC -! TISSUE SPECIFICITY: Expressed by the liver and secreted in plasma.

```
CC -!- SIMILARITY: Belongs to the serpin family.
DR PIR; A90345; A90345.
DR PDB; 3ER5; 15-JUL-92.
DR InterPro; IPR000215; Serpin.
DR PROSITE; PS00284; SERPIN; PARTIAL.
KW Vasoconstrictor; Plasma; Serpin; 3D-structure.
FT PEPTIDE 1 10 ANGIOTENSIN I.
FT PEPTIDE 1 8 ANGIOTENSIN II.
FT PEPTIDE 2 8 ANGIOTENSIN III.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1282 MW; CEEFDD761F2DB42 CRC64;

Query Match 22.0%; Score 13; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PF 9
Db 7 PF 8

RESULT 10
ANGT_CHICK STANDARD; PRT; 10 AA.
ID ANGT_CHICK
AC F01018;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Angiotensinogen (Contains: Angiotensin I (Ang I); Angiotensin II (Ang II); Angiotensin III (Ang III) (Des-Asp[1]-angiotensin II)) (Fragment).
DE AGT OR SERPINAS.
GN Gallus gallus (Chicken), and
OS Coturnix coturnix japonica (Japanese quail).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus
NCBI_TaxID=9031, 93934;
RX MEDLINE=74127845; PubMed=2191893;
RP SEQUENCE.
RC SPECIES=Chicken;
RA Nakayama T., Nakajima T., Sokabe H.;
RT "Comparative studies on angiotensins. 3. Structure of fowl
angiotensin and its identification by DNS-method.";
RL Chem. Pharm. Bull. 21:2085-2087(1973).
RN [2]
RP SEQUENCE.
RC SPECIES=C.c.japonica;
RX MEDLINE=90284684; PubMed=2191893;
RA Takei Y., Hasegawa Y.;
RT "Vasopressor and depressor effects of native angiotensins and
inhibition of these effects in the Japanese quail.";
RL Gen. Comp. Endocrinol. 79:12-22(1990).
CC -!- FUNCTION: In response to lowered blood pressure, the enzyme renin
cleaves angiotensin I, from angiotensinogen. ACE (angiotensin
converting enzyme) then removes a dipeptide to yield the
physiologically active peptide angiotensin II, the most potent
pressor substance known, which helps regulate volume and mineral
balance of body fluids.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the liver and secreted in plasma.
CC -!- SIMILARITY: Belongs to the serpin family.
DR PIR; A60624; A60624.
DR PIR; A90917; A90917.
DR InterPro; IPR000215; Serpin.
DR PROSITE; PS00284; SERPIN; PARTIAL.
KW Vasoconstrictor; Plasma; Serpin.
FT PEPTIDE 1 10 ANGIOTENSIN I.
FT PEPTIDE 1 8 ANGIOTENSIN II.
FT PEPTIDE 2 8 ANGIOTENSIN III.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1232 MW; CEEFDD761F2DB42 CRC64;

Query Match 22.0%; Score 13; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PF 9
Db 7 PF 8

RESULT 11
COXO_RAT STANDARD; PRT; 10 AA.
ID COXO_RAT
AC P80432;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytochrome c oxidase polypeptide VIIC, mitochondrial (EC 1.9.3.1)
DE (VIIIA) (Fragment).
GN COX7C OR COX7C1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
RX MEDLINE=95324529; PubMed=7601105;
RP SEQUENCE.
RC STRAIN=Wistar; TISSUE=Heart, and Liver;
RX Schaeffer H., Noack H., Halangk W., Brandt U., von Jagow G.;
RT "Cytochrome-c oxidase in developing rat heart. Enzymic properties and
amino-terminal sequences suggest identity of the fetal heart and the
adult liver isoform.";
RL Eur. J. Biochem. 230:235-241(1995).
CC -!- FUNCTION: This protein is one of the nuclear-coded polypeptide
chains of cytochrome c oxidase, the terminal oxidase in
mitochondrial electron transport.
CC -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
c + 2 H(2)O.
CC -!- SIMILARITY: Belongs to the cytochrome c oxidase VIIC family.
DR PIR; S65388; S65388.
KW Oxidoreductase; Mitochondrion.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1117 MW; 126DE767697B1B0B CRC64;

Query Match 22.0%; Score 13; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GP 8
Db 6 GP 7

RESULT 12
COXO_THUOB STANDARD; PRT; 10 AA.
ID COXO_THUOB
AC P80982;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cytochrome c oxidase polypeptide VIIC (EC 1.9.3.1) (Fragment).
OS Thunnus obesus (Bigeye tuna).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes; Scombroidei;
OC Scombridae; Thunnus.
NCBI_TaxID=8241;
RX MEDLINE=97454291; PubMed=9310366;
RA Arnold S., Lee I., Kim W., Song E., Linder D., Lottspeich F.,
Kadenbach B.;
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RT "The subunit structure of cytochrome-c oxidase from tuna heart and
RL liver."
CC Eur. J. Biochem. 248:99-103(1997).
CC -!- FUNCTION: This protein is one of the nuclear-coded polypeptide
CC chains of cytochrome c oxidase, the terminal oxidase in
CC mitochondrial electron transport.
CC -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
CC c + 2 H(2)O.
CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC -!- SIMILARITY: Belongs to the cytochrome c oxidase VIIC family.
CC DR PIR; S77990; S77990.
CC KW Oxidoreductase; Inner membrane; Mitochondrion.
CC FT NON_TER 10 10
CC SQ SEQUENCE 10 AA; 1059 MW; 126DE767687B1DCB CRC64;

Query Match 22.0%; Score 13; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GP 8
Db 6 GP 7

RESULT 13
PNEU_HUMAN
ID PNEU_HUMAN STANDARD; PRT; 10 AA.
AC P22103;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pneumadin (PNN).
OS Homo sapiens (Human).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Lung;
RX MEDLINE=91110910; PubMed=2274681;
RA Batra V.K., Mathur M., Mir S.A., Kapoor R., Kumar M.A.;
RT "Pneumadin: a new lung peptide which triggers antidiuresis.";
RL Regul. Pept. 30:77-87(1990).
CC -!- FUNCTION: Antidiuretic peptide that triggers the release of ADH.
CC DR PIR; B33143; B33143.
CC GO; GO:0030103; F:vasopressin secretion; NAS.
CC KW Amidation.
CC FT MOD_RES 10 10
CC SQ SEQUENCE 10 AA; 956 MW; 640378DAA723276B CRC64;

Query Match 22.0%; Score 13; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.2e+04;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 DSG 6
Db 7 DAG 9

RESULT 14
PNEU_RAT
ID PNEU_RAT STANDARD; PRT; 10 AA.
AC P21996;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pneumadin (PNN).
OS Rattus norvegicus (Rat).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
CC NCBI_TaxID=10116;
RN [1]
RP SEQUENCE, AND SYNTHESIS.

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RC TISSUE=Lung;
RX MEDLINE=91110910; PubMed=2274681;
RA Batra V.K., Mathur M., Mir S.A., Kapoor R., Kumar M.A.;
RT "Pneumadin: a new lung peptide which triggers antidiuresis.";
RL Regul. Pept. 30:77-87(1990).
CC -!- FUNCTION: This antidiuretic peptide triggers the release of ADH.
CC DR PIR; A33143; A33143.
CC KW Amidation.
CC FT MOD_RES 10 10
CC SQ SEQUENCE 10 AA; 1048 MW; 641D00DAA723276B CRC64;

Query Match 22.0%; Score 13; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.2e+04;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 DSG 6
Db 7 DAG 9

RESULT 15
RT02_BOVIN
ID RT02_BOVIN STANDARD; PRT; 10 AA.
AC P82923;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Mitochondrial 28S ribosomal protein S2 (MRP-S2) (Fragment).
GN MRPS2.
OS Bos taurus (Bovine).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
CC Bovidae; Bovinae; Bos.
CC NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=21276436; PubMed=11279123;
RA Koc E.C., Burkhardt W., Blackburn K., Moseley A., Spremulli L.L.;
RT "The small subunit of the mammalian mitochondrial ribosome:
RT identification of the full complement of ribosomal proteins present.";
RL J. Biol. Chem. 276:19363-19374(2001).
CC -!- SUBUNIT: Component of the mitochondrial ribosome small subunit
CC (28S) which comprises a 12S rRNA and about 30 distinct proteins.
CC -!- SUBCELLULAR LOCATION: Mitochondrial.
CC -!- SIMILARITY: Belongs to the S2P family of ribosomal proteins.
CC InterPro; IPR001865; Ribosomal S2.
CC PROSITE; PS00962; RIBOSOMAL_S2_1; PARTIAL.
CC KW Ribosomal protein; Mitochondrion.
CC FT NON_TER 1 1
CC FT NON_TER 10 10
CC SQ SEQUENCE 10 AA; 1246 MW; 6A7A6679C04B476B CRC64;

Query Match 22.0%; Score 13; DB 1; Length 10;
Best Local Similarity 33.3%; Pred. No. 1.2e+04;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 8 PFV 10
Db 4 PYI 6

Search completed: February 26, 2004, 09:22:04
Job time : 12.5 secs

```

GenCore version 5.1.6
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QM protein - protein search, using sw model

Run on: February 26, 2004, 09:16:49 ; Search time 35 Seconds
(without alignments)
90.148 Million cell updates/sec

Title: US-09-909-348-1
Perfect score: 59
Sequence: 1 CEGDGGPFV 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues
Total number of hits satisfying chosen parameters: 603

Minimum DB seq length: 10
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- SPTREMBL 25:*
- 1: sp_archaea:*
 - 2: sp_bacteria:*
 - 3: sp_fungi:*
 - 4: sp_human:*
 - 5: sp_invertebrate:*
 - 6: sp_mammal:*
 - 7: sp_mic:*
 - 8: sp_organelle:*
 - 9: sp_phage:*
 - 10: sp_plant:*
 - 11: sp_rodent:*
 - 12: sp_virus:*
 - 13: sp_vertebrate:*
 - 14: sp_unclassified:*
 - 15: sp_virus:*
 - 16: sp_bacteriopl:*
 - 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	23	39.0	10	P82938	P82938 hordeum vul
2	20	33.9	10	Q50032	Q50032 mycobacteri
3	20	33.9	10	Q9TS42	Q9TS42 sus scrofa
4	18	30.5	10	Q9UNF2	Q9UNF2 homo sapien
5	18	30.5	10	Q9QVK7	Q9QVK7 mus sp. nep
6	17	28.8	10	Q9X533	Q9X533 escherichia
7	17	28.8	10	Q9X534	Q9X534 leclercia a
8	17	28.8	10	Q9UE86	Q9UE86 homo sapien
9	17	28.8	10	Q947X7	Q947X7 solanum tub
10	16	27.1	10	Q9TU33	Q9TU33 canis famil
11	16	27.1	10	P82136	P82136 spinacia ol
12	16	27.1	10	Q8CJ31	Q8CJ31 mus musculu
13	15	25.4	10	Q9X3M2	Q9X3M2 prochloroco
14	15	25.4	10	Q96QA7	Q96QA7 homo sapien
15	15	25.4	10	Q8NEY9	Q8NEY9 homo sapien
16	15	25.4	10	Q9P2Z9	Q9P2Z9 homo sapien

17	15	25.4	10	10	Q9S936	Q9S936 beta vulgar
18	15	25.4	10	11	Q9QVFO	Q9QVFO mus sp. pro
19	15	25.4	10	11	Q9QVE9	Q9QVE9 mus sp. pro
20	14	23.7	10	4	Q8Q493	Q8Q493 homo sapien
21	14	23.7	10	5	P82222	P82222 bombyx mori
22	14	23.7	10	6	Q8MJ78	Q8MJ78 bos mutus g
23	14	23.7	10	10	Q99213	Q99213 aegilops sq
24	13	22.0	10	2	Q8KJF1	Q8KJF1 pseudomonas
25	13	22.0	10	2	Q9R7J8	Q9R7J8 helicobacte
26	13	22.0	10	4	Q9UCR0	Q9UCR0 homo sapien
27	13	22.0	10	4	Q81ZA2	Q81ZA2 homo sapien
28	13	22.0	10	8	Q8SH93	Q8SH93 brookesia p
29	13	22.0	10	8	Q8SHA8	Q8SHA8 rhampolsen
30	13	22.0	10	8	Q8SAZ9	Q8SAZ9 pyrrobrum
31	13	22.0	10	10	Q9FS93	Q9FS93 silene pent
32	13	22.0	10	10	Q7YOR0	Q7YOR0 brassica ju
33	13	22.0	10	11	Q63389	Q63389 rattus norv
34	13	22.0	10	12	Q83978	Q83978 influenzavi
35	13	22.0	10	12	P90373	P90373 suid herpes
36	13	22.0	10	13	Q9PRY8	Q9PRY8 triakis scy
37	13	22.0	10	13	Q9QY93	Q9QY93 gallus gall
38	13	22.0	10	13	Q9PS07	Q9PS07 alligator m
39	13	22.0	10	13	Q9PRU9	Q9PRU9 sparus aura
40	13	22.0	10	13	O73594	O73594 gallus gall
41	12	20.3	10	2	Q8KH99	Q8KH99 clostridium
42	12	20.3	10	2	Q52837	Q52837 rhizobium l
43	12	20.3	10	2	Q51812	Q51812 escherichia
44	12	20.3	10	4	Q9UCU6	Q9UCU6 homo sapien
45	12	20.3	10	4	Q7Z5A2	Q7Z5A2 homo sapien

ALIGNMENTS

RESULT 1

P82938 ID P82938 PRELIMINARY; PRT; 10 AA.
AC P82938; ID P82938; PRELIMINARY; PRT; 10 AA.
DT 01-MAR-2001 (TREMREL. 16, Created)
DT 01-MAR-2001 (TREMREL. 16, Last sequence update)
DT 01-JUN-2001 (TREMREL. 17, Last annotation update)
DE Unknown endospore protein C (Fragment).
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE.
RC STRAIN=cv. BOMI; TISSUE=Starchy endosperm;
RX MEDLINE=2108911; PubMed=11271488;
RA Kistoffersen H.E., Flengsrud R.;
RT "Separation and characterization of basic barley seed proteins.";
RL Electrophoresis 21:3693-3700(2000).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 8.5-9.0, ITS MW IS: 11.9 KDA.
FT NON TER 10
SQ SEQUENCE 10 AA; 1053 MW; 9E562DC40AA87AAE CRC64;

Query Match 39.0%; Score 23; DB 10; Length 10;
Best Local Similarity 75.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CEGD 4
Db 3 CDGD 6

RESULT 2

Q50032 ID Q50032 PRELIMINARY; PRT; 10 AA.
AC Q50032;
DT 01-NOV-1996 (TREMREL. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1996 (TrEMBLrel. 01, Last annotation update)
DE U22669.
OS Mycobacterium leprae.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=11769;
RN [1]
RP SEQUENCE FROM N.A.
RA Smith D.R.;
RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
RP [2]
RP SEQUENCE FROM N.A.
RA Robinson K.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; ULS182; AA62975.1;
SQ SEQUENCE 10 AA; 1137 MW; 5F3F317B1EB455B7 CRC64;

Query Match 33.9%; Score 20; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CEG 3
DB 6 CEG 8

RESULT 3
Q9TS42 PRELIMINARY; PRT; 10 AA.
AC Q9TS42;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE OESTRADIOL-RECEPTOR=P2 peptide (Fragment).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9923;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91291128; PubMed=2064608;
RA Thole H.H., Jungblut P.W., Jakob F.;
RT "The proton-driven dissociation of oestradiol-receptor dimers as a
preparative tool. Isolation of a 32 kDa fragment from porcine uteri
and assignment of C-terminal origin by partial sequencing.";
RL Biochem. J. 276:709-714(1991).
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 10 AA; 992 MW; D95E047B1451B76D CRC64;

Query Match 33.9%; Score 20; DB 6; Length 10;
Best Local Similarity 60.0%; Pred. No. 5.9e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 DSGGP 8
DB 6 NEGGP 10

RESULT 4
Q9UNF2 PRELIMINARY; PRT; 10 AA.
AC Q9UNF2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Alpha 1 collagen (Fragment).
GN COL1A1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;

RN SEQUENCE FROM N.A.
RP TISSUE=Breast;
RA Ratcliffe T.A., Vitz J.R., Ray D.B.;
RT "SNP located within intron 32 of human pro-alpha 1 (I) collagen gene
at 10,828 bp: cytosine replaces adenine";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF128441; AAD32608.1;
RN [1]
RP SEQUENCE FROM N.A.
RA Smith D.R.;
RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
RP [2]
RP SEQUENCE FROM N.A.
RA Robinson K.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; ULS182; AA62975.1;
SQ SEQUENCE 10 AA; 953 MW; 364F91A873276867 CRC64;

Query Match 30.5%; Score 18; DB 4; Length 10;
Best Local Similarity 60.0%; Pred. No. 1.3e+04;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 EGDGS 6
DB 6 KGDG 10

RESULT 5
Q9QVK7 PRELIMINARY; PRT; 10 AA.
AC Q9QVK7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE MEPRIN-METALLOENDOPEPTIDASE (Fragment).
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP SEQUENCE.
RX MEDLINE=91363409; PubMed=1888759;
RA Flannery A.V., Macadam G.C., Beynon R.J.;
RT "Immunological characterisation of different meprin species in mice.";
RL Biochim. Biophys. Acta 1079:119-122(1991).
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 10 AA; 1138 MW; FC01BFB5BAA866D1 CRC64;

Query Match 30.5%; Score 18; DB 11; Length 10;
Best Local Similarity 75.0%; Pred. No. 1.3e+04;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 EGDGS 5
DB 4 QGDS 7

RESULT 6
Q9X533 PRELIMINARY; PRT; 10 AA.
AC Q9X533;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Periplasmic mercuric ion binding protein (Fragment).
GN MERP.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=209A;
RC MEDLINE=97208220; PubMed=9055422;
RA Liebert C.A., Wireman J., Smith T., Summers A.O.;
RT "Phylogeny of mercury resistance (mer) operons of gram-negative
bacteria isolated from the fecal flora of primates.";

QY 2 EGDGS 5
DB 4 QGDS 7

```

RN Appl. Environ. Microbiol. 63:1066-1076(1997).
RP SEQUENCE FROM N.A.
RC STRAIN=209A;
RA MEDLINE=98027386; PubMed=9361435;
RX Wireman J., Liebert C.A., Smith T., Summers A.O.;
RT "Association of mercury resistance with antibiotic resistance in the
RL gram-negative fecal bacteria of primates.";
RN Appl. Environ. Microbiol. 63:4494-4503(1997).
RP SEQUENCE FROM N.A.
RC STRAIN=209A;
RX MEDLINE=20568355; PubMed=11116334;
RA Liebert C.A., Watson A.L., Summers A.O.;
RT "The quality of merC, a module of the mer mosaic.";
RL J. Mol. Evol. 51:607-622(2000).
DR EMBL; AF120964; AAD23783.1; -.
FT NON TER 1
SQ SEQUENCE 10 AA; 1093 MW; 3F526335A5A77B58 CRC64;

Query Match 28.8%; Score 17; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 2e+04;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 DSGGP 8
DB 1 DAGYP 5

RESULT 7
QX534 PRELIMINARY; PRT; 10 AA.
AC QX534;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Periplasmic mercuric ion binding protein (Fragment).
GN MERP.
OS Leclercia adacarboxylata.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Leclercia.
OX NCBI_TaxID=83655;
RN SEQUENCE FROM N.A.
RP STRAIN=742H;
RX MEDLINE=97208220; PubMed=90554422;
RA Liebert C.A., Wireman J., Smith T., Summers A.O.;
RT "Phylogeny of mercury resistance (mer) operons of gram-negative
RL bacteria isolated from the fecal flora of primates.";
RN Appl. Environ. Microbiol. 63:1066-1076(1997).
RP SEQUENCE FROM N.A.
RC STRAIN=742H;
RX MEDLINE=98027386; PubMed=9361435;
RA Wireman J., Liebert C.A., Smith T., Summers A.O.;
RT "Association of mercury resistance with antibiotic resistance in the
RL gram-negative fecal bacteria of primates.";
RN Appl. Environ. Microbiol. 63:4494-4503(1997).
RP SEQUENCE FROM N.A.
RC STRAIN=742H;
RX MEDLINE=20568355; PubMed=11116334;
RA Liebert C.A., Watson A.L., Summers A.O.;
RT "The quality of merC, a module of the mer mosaic.";
RL J. Mol. Evol. 51:607-622(2000).
DR EMBL; AF120965; AAD23785.1; -.
FT NON TER 1
SQ SEQUENCE 10 AA; 1093 MW; 3F526335A5A77B58 CRC64;

Query Match 28.8%; Score 17; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 2e+04;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 4 DSGGP 8
DB 1 DAGYP 5

RESULT 8
QX534 PRELIMINARY; PRT; 10 AA.
AC QX534;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Collagen alpha 1(I) chain (Fragment).
GN COL1A1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN SEQUENCE FROM N.A.
RP MEDLINE=92042176; PubMed=1939261;
RA Hawkins J.R., Superti-Furga A., Steinmann B., Dalglish R.;
RT "A 9-base pair deletion in COL1A1 in a lethal variant of osteogenesis
RL imperfecta.";
DR EMBL; S66556; AAB20361.1; -.
DR GO; GO:0005584; C:collagen type I; NAS.
DR GO; GO:0005201; P:extracellular matrix structural constituent; NAS.
DR GO; GO:0007155; P:cell adhesion; NAS.
FT NON TER 1
FT NON TER 10
SQ SEQUENCE 10 AA; 777 MW; 2D20F6D8676DD867 CRC64;

Query Match 28.8%; Score 17; DB 4; Length 10;
Best Local Similarity 50.0%; Pred. No. 2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DSGGP 8
DB 1 GPPGAP 6

RESULT 9
QX47R7 PRELIMINARY; PRT; 10 AA.
AC QX47R7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE SKT1 potassium channel (Fragment).
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4113;
RN SEQUENCE FROM N.A.
RP STRAIN=742H;
RX MEDLINE=98027386; PubMed=9361435;
RA Wireman J., Liebert C.A., Smith T., Summers A.O.;
RT "Association of mercury resistance with antibiotic resistance in the
RL gram-negative fecal bacteria of primates.";
RN Appl. Environ. Microbiol. 63:4494-4503(1997).
RP SEQUENCE FROM N.A.
RC STRAIN=742H;
RX MEDLINE=20568355; PubMed=11116334;
RA Liebert C.A., Watson A.L., Summers A.O.;
RT "The quality of merC, a module of the mer mosaic.";
RL J. Mol. Evol. 51:607-622(2000).
DR EMBL; AF120965; AAD23785.1; -.
FT NON TER 1
SQ SEQUENCE 10 AA; 1093 MW; 3F526335A5A77B58 CRC64;

Query Match 28.8%; Score 17; DB 10; Length 10;
Best Local Similarity 60.0%; Pred. No. 2e+04;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

DB 2 GDNRG 6

Query Match 27.1%; Score 16; DB 8; Length 10;
 Best Local Similarity 66.7%; Pred. No. 2.9e+04;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 PFV 10
 DB 7 PFI 9

RESULT 10

Q9TU33 PRELIMINARY; PRT; 10 AA.

ID Q9TU33;
 AC Q9TU33;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE BRCA1 (Fragment).
 GN BRCA1.

OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20154965; PubMed=10690375;
 RA Gray I.S., Yuzbasivan-Gurkan V.;
 RT "A single nucleotide (T-->G) polymorphism within intron 23 of the
 RL canine BRCA1 gene.";
 RL Anim. Genet. 31:76-77(2000).
 DR EMBL; AF159258; AAD56289.1; -.
 FT NON_TER 1
 FT NON_TER 10
 SQ SEQUENCE 10 AA; 1164 MW; 2AB89C65BAAB01B3 CRC64;

Query Match 27.1%; Score 16; DB 6; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.9e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DSG 6
 DB 6 DSG 8

RESULT 11

P82136 PRELIMINARY; PRT; 10 AA.

ID P82136;
 AC P82136;
 DT 01-JUN-2000 (TrEMBLrel. 14, Created)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Chloroplast 30S ribosomal protein S18 beta (Fragment).
 OS Spinacia oleracea (Spinach).
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllales; Amaranthaceae; Spinacia.
 OX NCBI_TaxID=3562;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=cv. ALVARO; TISSUE=Leaf;
 RX MEDLINE=20435797; PubMed=10874039;
 RA Yamaguchi K., von Knoblauch K., Subramanian A.R.;
 RT "The plastid ribosomal proteins. Identification of all the proteins in
 RT the small subunit of an organelle ribosome (chloroplast).";
 RL J. Biol. Chem. 37:28455-28465(2000).
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
 CC -1- MISCELLANEOUS: S18 ALPHA AND BETA FORMS DIFFER IN P.I. S18 BETA
 CC FORM IS THE LEAST BASIC FORM.
 CC -1- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 14 KDA.
 CC -1- SIMILARITY: BELONGS TO THE S1P FAMILY OF RIBOSOMAL PROTEINS.
 DR GO; GO:0009507; C:chloroplast; IEA.
 DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
 DR InterPro; IPR001648; Ribosomal_S18.
 DR PROSITE; PS00057; RIBOSOMAL_S18; PARTIAL.
 KW Ribosomal protein; Chloroplast.
 FT NON_TER 10
 FT NON_TER 10
 SQ SEQUENCE 10 AA; 1250 MW; 403B60D7740325B3 CRC64;

Query Match 27.1%; Score 16; DB 8; Length 10;
 Best Local Similarity 66.7%; Pred. No. 2.9e+04;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 PFV 10
 DB 3 PFI 5

RESULT 13

Q9X3M2 PRELIMINARY; PRT; 10 AA.

ID Q9X3M2;
 AC Q9X3M2;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
 DE Cytochrome b (Fragment).
 GN PETB.
 OS Prochlorococcus sp.
 OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
 OC Prochlorococcus.
 OX NCBI_TaxID=1220;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Urbach E., Chisholm S.W.;
 RT "Genetic diversity in Prochlorococcus populations flow cytometrically
 RT sorted from the Sargasso Sea and Gulf Stream.";
 RL Limnol. Oceanogr. 43:1615-1630(1998).
 DR EMBL; AF070219; AAD23269.1; -.
 FT NON_TER 1

Thu Feb 26 10:40:03 2004

Db 3 CGSYCCG 9

Search completed: February 26, 2004, 09:23:28
Job time : 39 secs

SO SEQUENCE 10 AA; 1076 MW; 75CA5CB05866D324 CRC64;
Query Match 25.4%; Score 15; DB 2; Length 10;
Best Local Similarity 60.0%; Pred.No. 4.3e+04;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 2 EGDSS 6
Db 5 QGISG 9

RESULT 14
Q96QA7 PRELIMINARY; PRT; 10 AA.
AC Q96QA7; 2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE BA151A2.1 (Cdc42 guanine exchange factor (GEF) 9 (Collypistin, PEM-2, HPEW-2, KIAA0424)) (Fragment).
GN ARHGEF9.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Whitehead S.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL451106; CAC89408.1; -.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1122 MW; 39925CB878640043 CRC64;

Query Match 25.4%; Score 15; DB 4; Length 10;
Best Local Similarity 75.0%; Pred.No. 4.3e+04;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GDSSG 6
Db 6 GGSG 9

RESULT 15
Q8NEY9 PRELIMINARY; PRT; 10 AA.
AC Q8NEY9;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Type II hair-specific keratin (Fragment).
GN KRTHB6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Bairwa N.K.; Banezai R.;
RT "Study of polymorphism in the regulatory region of KRTHB6 in monilethrix samples."
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY037552; AAK68688.1; -.
DR GO; GO:0005882; C:intermediate filament; IEA.
KW Keratin.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1034 MW; 9B53417EAB45B87E CRC64;

Query Match 25.4%; Score 15; DB 4; Length 10;
Best Local Similarity 42.9%; Pred.No. 4.3e+04;
Matches 3; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CEGDSSG 7
Db 1 CEGDSSG 7

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OM protein - protein search, using sw model

Run on: February 26, 2004, 09:00:54 ; Search time 48.5 seconds
(without alignments)
58.257 Million cell updates/sec

Title: US-09-909-348-1
Perfect score: 59
Sequence: 1 CEGDGGPFV 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 94656

Minimum DB seq length: 10
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	59	100.0	10	5 AAU78372	Serine es
2	59	100.0	10	5 AAE20155	Serine es
3	59	100.0	10	7 ABB80261	Serine es
4	46	78.0	10	5 AAU78373	Serine es
5	46	78.0	10	5 AAE20156	Serine es
6	46	78.0	10	7 ABB80262	Serine es
7	43	72.9	10	4 AAB35464	Human mem
8	34	57.6	10	4 AAG94412	Human mem
9	31	52.5	10	4 AAJ01260	Hepatitis
10	30	50.8	10	2 AAR61594	Peptide f
11	30	50.8	10	4 AAJ00701	Hepatitis
12	30	50.8	10	4 AAJ01934	Hepatitis
13	30	50.8	10	4 AAJ01082	Hepatitis
14	29	49.2	10	2 AAR11746	Cyclic pl
15	29	49.2	10	2 AAR11747	Cyclic pl
16	29	49.2	10	2 AAR96844	N-gonorrh
17	29	49.2	10	2 AAW79650	N-alpha-A
18	29	49.2	10	2 AAW79652	N-alpha-A
19	29	49.2	10	2 AAW79651	N-alpha-A
20	29	49.2	10	6 ABR26505	Human can
21	29	49.2	10	6 ABR26505	Human can
22	29	49.2	10	6 ABR26550	Human can
23	29	49.2	10	6 ABR26548	Human can
24	29	49.2	10	6 ABR25883	Human can
25	28	47.5	10	4 AAG97390	Human can

26	28	47.5	10	7 ADD69406	Angiopoie
27	27	45.8	10	3 AAB26630	Partial s
28	27	45.8	10	4 AAG97589	Human com
29	27	45.8	10	4 AAG97590	Human com
30	27	45.8	10	4 AAB49021	IL-6R-der
31	27	45.8	10	4 AAB49022	IL-6R-der
32	27	45.8	10	5 AAE24304	Human E-c
33	27	45.8	10	5 AAE28776	Human CAS
34	26	44.1	10	2 AAW23020	R1 recept
35	25	42.4	10	2 AAR10181	RGD-contg
36	25	42.4	10	2 AAR76887	Glutathio
37	25	42.4	10	2 AAW05434	GST-bind
38	25	42.4	10	2 AAW03419	Fibronect
39	25	42.4	10	2 AAW48515	Integrin
40	25	42.4	10	2 AAY47394	Immunogen
41	25	42.4	10	2 AAY46325	Immunogen
42	25	42.4	10	2 AAY46326	Immunogen
43	25	42.4	10	2 AAG93857	Human com
44	25	42.4	10	4 AAG93980	Human com
45	25	42.4	10	4 AAG95897	Human com

ALIGNMENTS

RESULT 1

AAU78372
ID AAU78372 standard; peptide; 10 AA.
XX
AC AAU78372;
XX
DT 18-JUN-2002 (first entry)
XX
DE Serine esterase conserved sequence #1.
XX
KW Serine esterase; osteopathic; thrombin; receptor; agonist;
KW bone growth stimulation; osteoinduction; farm animal; companion animal;
KW laboratory animal; bone graft; segmental bone gap; bone void;
KW non-union fracture.
XX
OS Synthetic.
XX
PN WO200205836-A2.
XX
PD 24-JAN-2002.
XX
PF 18-JUL-2001; 2001WO-US022641.
XX
PR 19-JUL-2000; 2000US-0219300P.
XX
PA (TEXA) UNIV TEXAS SYSTEM.
XX
PI Carney DH, Crowther RS, Simmons DJ, Yang J, Redin WR;
XX
DR WPI; 2002-303796/34.
XX
PT Stimulating bone growth at a site in a subject in need of osteoinduction,
PT such as a site of bone graft, segmental bone gap, bone void or non-union
PT structure, by administering agonist of activated thrombin receptor.
XX
PS Claim 6; Page 21; 27pp; English.
XX
CC The invention describes a method of stimulating bone growth at a site in
CC a subject in need of osteoinduction. The method involves administering an
CC agonist to stimulate bone growth at a site in a subject (e.g. a farm
CC animal, companion animal or laboratory animal), in need of
CC osteoinduction, such as the site in need of a bone graft in a subject, a
CC segmental bone gap, a bone void or a non-union fracture. This sequence
CC represents a serine esterase conserved sequence obtained from a serine
CC esterase that can stimulate or activate the non-proteolytically activated
CC thrombin receptor
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 59; DB 5; Length 10;
 Best Local Similarity 100.0%; Pred. NO. 0.12;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CEGDSGGPFV 10
 DB 1 CEGDSGGPFV 10

RESULT 2
 AAE20155
 ID AAE20155 standard; peptide; 10 AA.
 XX
 AC AAE20155;
 XX
 DT 18-JUN-2002 (first entry)
 XX
 DE Serine esterase conserved peptide #1.
 XX
 KW Cartilage growth; cartilage repair; arthritic joint; traumatic injury;
 KW non-proteolytically activated thrombin receptor; NPAR; chondrocyte;
 KW therapy; implantation; serine esterase conserved peptide.
 XX
 OS Unidentified.
 XX
 FN WO200207748-A2.
 XX
 PD 31-JAN-2002.
 XX
 PF 19-JUL-2001; 2001WO-US022668.
 XX
 PR 20-JUL-2000; 2000US-0219800P.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 PI Carney DH, Crowther RS, Stiernberg J, Bergmann J;
 XX WPI; 2002-268953/31.
 DR
 XX
 PT Stimulating growth and repair of cartilage, useful for treating e.g.
 PT arthritis, by local administration of an agonist of non-proteolytically
 PT activated thrombin receptor.
 XX
 PS Claim 7; Page 24; 28pp; English.
 XX
 CC The invention relates to a method of stimulating growth and repair of
 CC cartilage. The method involves administering to the site, an agonist of
 CC non-proteolytically activated thrombin receptor (NPAR). The method is
 CC used in human or veterinary medicine for the treatment of arthritic
 CC joints and damage/loss of cartilage caused by traumatic injury. Also
 CC chondrocytes may be cultured in presence of NPAR agonist to provide cells
 CC for implantation at sites requiring growth/repair of cartilage. The
 CC present sequence is serine esterase conserved peptide. This sequence is
 CC present in the thrombin peptide derivatives which serve as a NPAR agonist
 XX
 SQ Sequence 10 AA;

Query Match 100.0%; Score 59; DB 5; Length 10;
 Best Local Similarity 100.0%; Pred. NO. 0.12; 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CEGDSGGPFV 10
 DB 1 CEGDSGGPFV 10

RESULT 3
 ABB80261
 ID ABB80261 standard; peptide; 10 AA.
 XX
 AC ABB80261;
 XX

DT 18-DEC-2003 (first entry)
 XX
 DE Serine esterase conserved sequence #1.
 XX
 KW Serine esterase; conserved domain; thrombin peptide; stimulation; bone;
 KW cartilage; growth; repair; bone graft; segmental gap; bone void;
 KW non-union fracture; arthritic joint; arthritis; damage; traumatic injury;
 KW culture; chondrocyte; joint bio mechanics; osteoarthritis.
 XX
 OS Mammal sp.
 XX
 FN WO2003061690-A1.
 XX
 PD 31-JUL-2003.
 XX
 PF 17-JAN-2002; 2002WO-US001451.
 XX
 PR 17-JAN-2002; 2002WO-US001451.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 PI Carney DH, Crowther RS, Simmons DJ, Yang J, Redin WR;
 PI Stiernberg J, Bergmann J;
 XX
 DR WPI; 2003-721552/68.
 XX
 XX Stimulation of bone growth and cartilage formation in e.g. bone graft and
 PT arthritic joints involves administration of a thrombin derivative
 PT peptide.
 XX
 PS Disclosure; Page 8; Opp; English.
 XX
 CC The sequences given in ABB80261-62 represent serine esterase conserved
 CC domains. These peptide are used as part of the thrombin peptides
 CC derivatives of the invention for stimulating bone growth. The thrombin
 CC peptides of the invention have the formula: Asp-Ala-R, where R is a
 CC serine esterase conserved domain. These peptides are used for stimulating
 CC bone growth and cartilage growth or repair in e.g. bone graft, segmental
 CC gap in a bone, bone void, at a non-union fracture, arthritic injury, and
 CC sites treated for cartilage damage or loss due to traumatic injury, and
 CC for culturing chondrocytes in vitro. The thrombin derivative peptide
 CC improves the quality of repair tissue, leads to more durable and
 CC functional restoration of joint bio mechanics, reduces the incidence of
 CC osteoarthritis in patients suffering from traumatic cartilage injuries
 CC and accelerates the rate of normal fracture healing in fracture or small
 CC gap defects
 XX
 SQ Sequence 10 AA;

Query Match 100.0%; Score 59; DB 7; Length 10;
 Best Local Similarity 100.0%; Pred. NO. 0.12; 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CEGDSGGPFV 10
 DB 1 CEGDSGGPFV 10

RESULT 4
 AAU78373
 ID AAU78373 standard; peptide; 10 AA.
 XX
 AC AAU78373;
 XX
 DT 18-JUN-2002 (first entry)
 XX
 DE Serine esterase conserved sequence #2.
 XX
 KW Serine esterase; osteopathic; thrombin; receptor; agonist;
 KW bone growth stimulation; osteoinduction; farm animal; companion animal;
 KW laboratory animal; bone graft; segmental bone gap; bone void;
 KW non-union fracture.
 XX

PI Stiernberg J, Bergmann J;
XX WPI; 2003-721552/68.
XX
XX Stimulation of bone growth and cartilage formation in e.g. bone graft and
PT arthritic joints involves administration of a thrombin derivative
PT peptide.
XX
XX Disclosure; Page 8; Opp; English.
XX
XX The sequences given in ABB0261-62 represent serine esterase conserved
CC domains. These peptide are used as part of the thrombin peptides
CC derivatives of the invention for stimulating bone growth. The thrombin
CC peptides of the invention have the formula: Asp-Ala-R, where R is a
CC serine esterase conserved domain. These peptides are used for stimulating
CC bone growth and cartilage growth or repair in e.g. bone graft, segmental
CC gap in a bone, bone void, at a non-union fracture, arthritic joints, and
CC sites treated for cartilage damage or loss due to traumatic injury, and
CC for culturing chondrocytes in vitro. The thrombin derivative peptide
CC improves the quality of repair tissue, leads to more durable and
CC functional restoration of joint bio mechanics, reduces the incidence of
CC osteoarthritis in patients suffering from traumatic cartilage injuries
CC and accelerates the rate of normal fracture healing in fracture or small
CC gap defects
XX
XX Sequence 10 AA;
SQ
Query Match 78.0%; Score 46; DB 7; Length 10;
Best Local Similarity 80.0%; Pred. No. 6.9;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CEGDSGGPFV 10
DB 1 CXGDSGGPXV 10
RESULT 7
AAB35464
ID AAB35464 standard; protein; 10 AA.
XX
XX AAB35464;
XX
XX 06-JUN-2001 (first entry)
XX
XX Human membrane-type serine protease MT-SP1 PCR primer encoded peptide #2.
XX
XX Human; membrane-type serine protease; MT-SP1; cancer; PCR primer.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FT Misc-difference 2 /label= Ala, Ser, Thr
FT Misc-difference 4 /label= Lys, Glu, Gln, His
FT
XX
XX W0200123524-A2.
XX
XX 05-APR-2001.
XX
XX 02-OCT-2000; 2000WO-US027250.
XX
XX 30-SEP-1999; 99US-00410362.
XX
XX (REGC) UNIV CALIFORNIA.
XX
XX Craik CS, Takeuchi T, Shuman M;
XX
XX WPI; 2001-245002/25.
XX
XX N-PSDB; AAF28096.
XX
XX New nucleic acid encoding a membrane type serine protease, useful for the
PT diagnosis, prognosis and treatment of cancer, particularly metastatic

PT cancers.
XX
XX Example 1; Page 71; 102pp; English.
XX
XX The present invention provides the protein and coding sequences for the
CC novel human membrane-type serine protease MT-SP1. Increased expression of
CC this protein is associated with cancer, and so the sequences can be used
CC in cancer diagnosis and the identification of treatments. The present
CC sequence is a peptide encoded by a PCR primer used to isolate the MT-SP1
CC coding sequence
XX
XX Sequence 10 AA;
SQ
Query Match 72.9%; Score 43; DB 4; Length 10;
Best Local Similarity 87.5%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CEGDSGGP 8
DB 3 CXGDSGGP 10
RESULT 8
AAG94412
ID AAG94412 standard; peptide; 10 AA.
XX
XX AAG94412;
XX
XX 18-SEP-2001 (first entry)
XX
XX Human complementary peptide, SEQ ID NO: 606.
XX
XX Human; complementary peptide; ligand; drug discovery; drug design.
XX
XX Homo sapiens.
XX
XX W0200142277-A2.
XX
XX 14-JUN-2001.
XX
XX 13-DEC-2000; 2000WO-GB004776.
XX
XX 13-DEC-1999; 99GB-00029464.
XX
XX (PROT-) PROTEOM LTD.
XX
XX Roberts GW, Heal JR;
XX
XX WPI; 2001-408419/43.
XX
XX A set of peptide ligands consisting of specific complementary peptides to
PT proteins encoded by genes of the human genome, useful in an assay for
PT screening and identifying of one or more novel peptides which are drug
PT candidates or pro-drugs.
XX
XX Example 4; Page 126; 646pp; English.
XX
XX The invention relates to a set of complementary peptide ligands generated
CC from the human genome. The complementary peptides interact with their
CC relevant target proteins encoded in the human genome. They can be used as
CC reagents in drug discovery and as lead ligands to facilitate drug design
CC and development. The present sequence is a complementary peptide provided
CC in the specification
XX
XX Sequence 10 AA;
SQ
Query Match 57.6%; Score 34; DB 4; Length 10;
Best Local Similarity 71.4%; Pred. No. 2.9e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 CEGDSGG 7
DB 2 CKGESGG 8

```

RESULT 9
AAJ01260
ID AAJ01260 standard; peptide; 10 AA.
XX AC AAJ01260;
XX DT 02-JUL-2001 (first entry)
XX DE Hepatitis C virus epitope #1251.
XX KW Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
XX KW antiviral.
XX OS Hepatitis C virus.
XX PN WO200121189-A1.
XX PD 29-MAR-2001.
XX PF 19-JUL-2000; 2000WO-US019774.
XX PR 19-JUL-1999; 99US-00357737.
XX PA (EPIM-) EPIMMUNE INC.
XX PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
XX PI Baker DM, Cells E, Kubo RT, Grey HM;
XX DR WPI; 2001-308046/32.
XX PT A new composition useful as a vaccine against hepatitis C virus.
XX PS Disclosure; Page 132; 214pp; English.
XX CC The present invention describes a composition comprising a prepared
CC hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
CC These are derived from HCV HLA-binding motifs. They are useful in
CC vaccines for the prevention and treatment of HCV infection in humans. The
CC present sequence is an epitope used in the disclosure of the invention
XX SQ Sequence 10 AA;
Query Match 52.5%; Score 31; DB 4; Length 10;
Best Local Similarity 55.6%; Pred. No. 7.5e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
OY 2 EGDGGPPV 10
DB 2 KGSSGGPLL 10
RESULT 10
AAJ01594
ID AAR61594 standard; peptide; 10 AA.
XX AC AAR61594;
XX DT 25-MAR-2003 (revised)
XX DT 12-MAY-1995 (first entry)
XX DE Peptide fragment (1.0479) of HCV binds HLA-A2.1.
XX KW antigen; epitope; immunogenic target protein; PSA; HBVC; HBVS; EBV; HIV1;
XX KW plasma specific antigen; hepatitis B virus; Epstein Barr;
XX KW human immunodeficiency virus; human papilloma virus; p53; c-PRB2; MAGE-1;
XX KW melanoma antigen-1; core antigen; surface antigen;
XX KW pharmaceutical composition; in vivo; ex vivo; therapeutic; diagnostic;
XX KW MHC class I molecule; major histocompatibility complex; HLA-A2.1; 9mer;
XX KW 10mer; anchor; human leukocyte antigen.
XX OS Hepatitis C virus.
Query Match 50.8%; Score 30; DB 2; Length 10;
Best Local Similarity 71.4%; Pred. No. 1e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
OY 2 EGDGGGP 8
DB 3 KGSSGGP 9
RESULT 11
AAJ00701
ID AAJ00701 standard; peptide; 10 AA.
XX AC AAJ00701;
XX DT 02-JUL-2001 (first entry)
XX DE Hepatitis C virus epitope #692.
XX KW Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
XX KW antiviral.
XX OS Hepatitis C virus.
XX PN WO200121189-A1.
XX PD 29-MAR-2001.
XX PF 19-JUL-2000; 2000WO-US019774.
XX PR 19-JUL-1999; 99US-00357737.
XX PA (EPIM-) EPIMMUNE INC.
XX PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
XX PI Baker DM, Cells E, Kubo RT, Grey HM;
XX DR WPI; 2001-308046/32.
XX PT A new composition useful as a vaccine against hepatitis C virus.
XX PS Disclosure; Page 132; 214pp; English.
XX CC The present invention describes a composition comprising a prepared
XX hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
XX These are derived from HCV HLA-binding motifs. They are useful in
XX vaccines for the prevention and treatment of HCV infection in humans. The
XX present sequence is an epitope used in the disclosure of the invention
XX SQ Sequence 10 AA;
Query Match 50.8%; Score 30; DB 2; Length 10;
Best Local Similarity 71.4%; Pred. No. 1e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
OY 2 EGDGGGP 8
DB 3 KGSSGGP 9

```

WO9420127-A1.

15-SEP-1994.

04-MAR-1994; 94WO-US002353.

05-MAR-1993; 93US-00027146.

04-JUN-1993; 93US-00073205.

29-NOV-1993; 93US-00159184.

(CYTE-) CYTEL CORP.

Grey HM, Sette A, Sidney J, Kast W;

WPI; 1994-302678/37.

Immunogenic peptide(s) having an HLA-A2.1 binding motif - used for treatment or prophylaxis of cancer, virus infection or autoimmune diseases.

Example 5; Page 111; 138pp; English.

AAR59496-R61666 are immunogenic 10mer peptides that contain a HLA-A2.1 binding motif. These peptides bind HLA-A2.1 and have a binding affinity of at least 1% as compared to a reference peptide (AAR1293). AAR61594 has an IC50 of 0.0002 and the sequence occurs at position 1160 in the HCV LORF protein. The peptides of the invention can induce cytotoxic T lymphocytes which can react with target cells. They can be used for the treatment or prophylaxis of cancer, eg. prostate cancer or lymphoma, etc. (Updated on 25-MAR-2003 to correct PN field.)

Sequence 10 AA;

Query Match 50.8%; Score 30; DB 2; Length 10;

Best Local Similarity 71.4%; Pred. No. 1e+03;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 EGDGGGP 8

DB 3 KGSSGGP 9

RESULT 11

AAJ00701

ID AAJ00701 standard; peptide; 10 AA.

AC AAJ00701;

DT 02-JUL-2001 (first entry)

DE Hepatitis C virus epitope #692.

KW Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;

KW antiviral.

OS Hepatitis C virus.

PN WO200121189-A1.

PD 29-MAR-2001.

PF 19-JUL-2000; 2000WO-US019774.

PR 19-JUL-1999; 99US-00357737.

PA (EPIM-) EPIMMUNE INC.

PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;

PI Baker DM, Cells E, Kubo RT, Grey HM;

DR WPI; 2001-308046/32.

PT A new composition useful as a vaccine against hepatitis C virus.

PS Disclosure; Page 132; 214pp; English.

CC The present invention describes a composition comprising a prepared

hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.

These are derived from HCV HLA-binding motifs. They are useful in

vaccines for the prevention and treatment of HCV infection in humans. The

present sequence is an epitope used in the disclosure of the invention

SQ Sequence 10 AA;

Query Match 52.5%; Score 31; DB 4; Length 10;

Best Local Similarity 55.6%; Pred. No. 7.5e+02;

Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 EGDGGPPV 10

DB 2 KGSSGGPLL 10

RESULT 10

AAJ01594

ID AAR61594 standard; peptide; 10 AA.

AC AAR61594;

DT 25-MAR-2003 (revised)

DT 12-MAY-1995 (first entry)

DE Peptide fragment (1.0479) of HCV binds HLA-A2.1.

KW antigen; epitope; immunogenic target protein; PSA; HBVC; HBVS; EBV; HIV1;

KW plasma specific antigen; hepatitis B virus; Epstein Barr;

KW human immunodeficiency virus; human papilloma virus; p53; c-PRB2; MAGE-1;

KW melanoma antigen-1; core antigen; surface antigen;

KW pharmaceutical composition; in vivo; ex vivo; therapeutic; diagnostic;

KW MHC class I molecule; major histocompatibility complex; HLA-A2.1; 9mer;

KW 10mer; anchor; human leukocyte antigen.

OS Hepatitis C virus.

PT A new composition useful as a vaccines against hepatitis C virus.
XX Disclosure; Page 117; 214pp; English.

CC The present invention describes a composition comprising a prepared
CC hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
CC These are derived from HCV HLA-binding motifs. They are useful in
CC vaccines for the prevention and treatment of HCV infection in humans. The
CC present sequence is an epitope used in the disclosure of the invention
XX Sequence 10 AA;

Query Match 50.8%; Score 30; DB 4; Length 10;
Best Local Similarity 71.4%; Pred. No. 1e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 EGDGGGP 8
:|||||
Db 3 KGSSGGP 9

RESULT 12
AAJ01934
ID AAJ01934 standard; peptide; 10 AA.

AC AAJ01934;
XX
XX 02-JUL-2001 (first entry)
XX Hepatitis C virus epitope #1925.
XX Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
XX antiviral.

OS Hepatitis C virus.
XX
XX WO200121189-A1.
XX
XX 29-MAR-2001.

XX 19-JUL-2000; 2000WO-US019774.
XX
XX 19-JUL-1999; 99US-00357737.
XX (EPIM-) EPIMUNE INC.
XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Cells E, Kubo RT, Grey HM;
XX WPI; 2001-308046/32.

XX A new composition useful as a vaccines against hepatitis C virus.
XX Disclosure; Page 148; 214pp; English.

CC The present invention describes a composition comprising a prepared
CC hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
CC These are derived from HCV HLA-binding motifs. They are useful in
CC vaccines for the prevention and treatment of HCV infection in humans. The
CC present sequence is an epitope used in the disclosure of the invention
XX Sequence 10 AA;

Query Match 50.8%; Score 30; DB 4; Length 10;
Best Local Similarity 71.4%; Pred. No. 1e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 EGDGGGP 8
:|||||
Db 3 KGSSGGP 9

RESULT 13

AAJ01082
ID AAJ01082 standard; peptide; 10 AA.
XX
AC AAJ01082;

XX 02-JUL-2001 (first entry)
XX Hepatitis C virus epitope #1073.
XX Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
XX antiviral.

XX Hepatitis C virus.
XX WO200121189-A1.
XX 29-MAR-2001.
XX 19-JUL-2000; 2000WO-US019774.
XX 19-JUL-1999; 99US-00357737.

XX (EPIM-) EPIMUNE INC.
XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Cells E, Kubo RT, Grey HM;
XX WPI; 2001-308046/32.
XX A new composition useful as a vaccines against hepatitis C virus.
XX Disclosure; Page 127; 214pp; English.

XX The present invention describes a composition comprising a prepared
XX hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
XX These are derived from HCV HLA-binding motifs. They are useful in
XX vaccines for the prevention and treatment of HCV infection in humans. The
XX present sequence is an epitope used in the disclosure of the invention
XX Sequence 10 AA;

Query Match 50.8%; Score 30; DB 4; Length 10;
Best Local Similarity 71.4%; Pred. No. 1e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 EGDGGGP 8
:|||||
Db 3 KGSSGGP 9

RESULT 14
AAJ11746
ID AAJ11746 standard; peptide; 10 AA.

XX
AC AAJ11746;
XX 25-MAR-2003 (revised)
XX 05-JUL-1991 (first entry)
XX Cyclic platelet aggregation inhibitor - example #3.
XX Myocardial infarction; deep vein thrombosis; pulmonary embolism; stroke.

XX Synthetic.
XX EP425212-A.
XX 02-MAY-1991.

XX 22-OCT-1990; 90EP-00311537.
XX 23-OCT-1989; 89US-00425906.

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OM protein - protein search, using sw model

Run on: February 26, 2004, 09:23:35 ; Search time 26.5 Seconds
(without alignments)
79.680 Million cell updates/sec

Title: US-09-909-348-1
Perfect score: 59
Sequence: 1 CEGDSGGPFFV 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 809742 seqs, 211153259 residues

Total number of hits satisfying chosen parameters: 31379

Minimum DB seq length: 10
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
 - 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
 - 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
 - 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
 - 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
 - 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
 - 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
 - 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
 - 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
 - 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
 - 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
 - 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
 - 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
 - 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
 - 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
 - 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
 - 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
 - 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	59	100.0	10	9	US-09-909-348-1
2	59	100.0	10	9	US-09-909-122-1
3	59	100.0	10	13	US-10-050-692-1
4	59	100.0	10	13	US-10-050-688-1
5	46	78.0	10	9	US-09-909-348-2
6	46	78.0	10	9	US-09-909-122-2
7	46	78.0	10	13	US-10-050-692-2
8	46	78.0	10	13	US-10-050-688-2
9	34	57.6	10	10	US-09-572-404B-606
10	28	47.5	10	10	US-09-572-404B-3584
11	27	45.8	10	10	US-09-572-404B-3784
12	27	45.8	10	10	US-09-572-404B-3785
13	25	42.4	10	9	US-09-879-957-55
14	25	42.4	10	10	US-09-572-404B-51
15	25	42.4	10	10	US-09-572-404B-53

16	25	42.4	10	10	US-09-572-404B-55	Sequence 55, Appl
17	25	42.4	10	10	US-09-572-404B-53	Sequence 63, Appl
18	25	42.4	10	10	US-09-572-404B-174	Sequence 174, Appl
19	25	42.4	10	10	US-09-572-404B-2027	Sequence 2027, App
20	25	42.4	10	10	US-09-572-404B-2033	Sequence 2033, Ap
21	25	42.4	10	10	US-09-572-404B-2091	Sequence 2091, Ap
22	25	42.4	10	10	US-09-572-404B-2093	Sequence 2093, Ap
23	25	42.4	10	10	US-09-572-404B-2095	Sequence 2095, Ap
24	25	42.4	10	10	US-09-572-404B-2098	Sequence 2098, Ap
25	25	42.4	10	10	US-09-932-165-319	Sequence 319, App
26	25	42.4	10	10	US-09-932-165-532	Sequence 532, App
27	25	42.4	10	10	US-09-932-165-745	Sequence 745, App
28	25	42.4	10	10	US-09-932-165-928	Sequence 928, App
29	25	42.4	10	10	US-09-932-165-1084	Sequence 1084, Ap
30	24	40.7	10	9	US-09-765-086-58	Sequence 58, Appl
31	24	40.7	10	10	US-09-572-404B-4	Sequence 4, Appl
32	24	40.7	10	10	US-09-572-270A-277	Sequence 277, App
33	24	40.7	10	10	US-09-572-270A-281	Sequence 281, App
34	24	40.7	10	10	US-09-572-270A-283	Sequence 283, App
35	24	40.7	10	10	US-09-572-270A-285	Sequence 285, App
36	24	40.7	10	10	US-09-572-270A-293	Sequence 293, App
37	24	40.7	10	10	US-09-572-270A-295	Sequence 295, App
38	24	40.7	10	13	US-10-008-355-25	Sequence 25, Appl
39	24	40.7	10	14	US-10-264-374-58	Sequence 58, Appl
40	24	40.7	10	14	US-10-375-992-58	Sequence 58, Appl
41	23	39.0	10	10	US-09-572-404B-114	Sequence 114, App
42	23	39.0	10	10	US-09-572-404B-176	Sequence 176, App
43	23	39.0	10	10	US-09-572-404B-342	Sequence 342, App
44	23	39.0	10	10	US-09-572-404B-344	Sequence 344, App
45	23	39.0	10	10	US-09-572-404B-1306	Sequence 1306, Ap

ALIGNMENTS

RESULT 1
US-09-909-348-1
; Sequence 1, Application US/09909348
; Patent No. US20020042373A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; APPLICANT: Crowther, Roger S.
; APPLICANT: Stierberg, Janet
; APPLICANT: Bergmann, John
; TITLE OF INVENTION: Stimulation Of Cartilage Growth With Agonists
; TITLE OF INVENTION: Of The No. US20020042373A1-Proteolytically Activated Thrombin Re
; FILE REFERENCE: 3033.1003-001
; CURRENT APPLICATION NUMBER: US/09/909,348
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/219,800
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide fragment of Thrombin
US-09-909-348-1

Query Match 100.0%; Score 59; DB 9; Length 10;
Best Local Similarity 100.0%; Fred. No. 0.0057;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CEGDSGGPFFV 10
Db 1 CEGDSGGPFFV 10

RESULT 2
US-09-909-122-1
; Sequence 1, Application US/09909122

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; Patent No. US20020128202A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; APPLICANT: Crowther, Roger S.
; APPLICANT: Simmons, David J.
; APPLICANT: Yang, Jinning
; APPLICANT: Redin, William R.
; TITLE OF INVENTION: Stimulation Of Bone Growth With Thrombin
; TITLE OF INVENTION: Peptide Derivatives
; FILE REFERENCE: 3033.1002-001
; CURRENT APPLICATION NUMBER: US/09/909,122
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/219,300
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide fragment of Thrombin
US-09-909-122-1
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Query Match 100.0%; Score 59; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0057;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CEGDSGGPFV 10
Db 1 CEGDSGGPFV 10
|||||
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RESULT 3

US-10-050-692-1

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; Sequence 1, Application US/10050692
; Publication No. US20020182205A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; APPLICANT: Crowther, Roger S.
; APPLICANT: Simmons, David J.
; APPLICANT: Yang, Jinning
; APPLICANT: Redin, William R.
; TITLE OF INVENTION: STIMULATION OF BONE GROWTH WITH THROMBIN
; TITLE OF INVENTION: PEPTIDE DERIVATIVES
; FILE REFERENCE: 3033.1002-004
; CURRENT APPLICATION NUMBER: US/10/050,692
; CURRENT FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: 09/909,122
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/219,300
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fragment of human prothrombin
US-10-050-692-1
```

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Query Match 100.0%; Score 59; DB 13; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0057;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CEGDSGGPFV 10
Db 1 CEGDSGGPFV 10
|||||
```

RESULT 4

US-10-050-688-1

```
; Sequence 1, Application US/10050688
; Publication No. US20020198154A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; APPLICANT: Crowther, Roger S.
; APPLICANT: Stierberg, Janet
; APPLICANT: Bergmann, John
; TITLE OF INVENTION: STIMULATION OF CARTILAGE GROWTH WITH
; TITLE OF INVENTION: AGONISTS OF THE NON-PROTEOLYTICALLY ACTIVATED THROMBIN
; TITLE OF INVENTION: RECEPTOR
; FILE REFERENCE: 3033.1003-004
; CURRENT APPLICATION NUMBER: US/10/050,688
; CURRENT FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: 09/909,348
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/219,800
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide fragment of thrombin
US-10-050-688-1
```

```
Query Match 100.0%; Score 59; DB 13; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0057;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 CEGDSGGPFV 10
Db 1 CEGDSGGPFV 10
|||||
```

RESULT 5

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US-09-909-348-2
; Sequence 2, Application US/09909348
; Patent No. US20020042373A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; APPLICANT: Crowther, Roger S.
; APPLICANT: Stierberg, Janet
; APPLICANT: Bergmann, John
; TITLE OF INVENTION: Stimulation Of Cartilage Growth With Agonists
; TITLE OF INVENTION: Of The No. US20020042373A1-Proteolytically Activated Thrombin Re
; FILE REFERENCE: 3033.1003-001
; CURRENT APPLICATION NUMBER: US/09/909,348
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/219,800
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide fragment of Thrombin
; NAME/KEY: VARIANT
; LOCATION: (1)...(10)
; OTHER INFORMATION: Xaa at position two is Glu or Gln
; OTHER INFORMATION: Xaa at position nine is Phe, Met, Leu, His or Val
US-09-909-348-2
```

```
Query Match 78.0%; Score 46; DB 9; Length 10;
Best Local Similarity 80.0%; Pred. No. 0.62;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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```
QY 1 CEGDSGGPFV 10
Db 1 CEGDSGGPFV 10
|||||
```

```

RESULT 6
US-09-909-122-2
; Sequence 2, Application US/09909122
; Patent No. US20020128202A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; APPLICANT: Crowther, Roger S.
; APPLICANT: Simmons, David J.
; APPLICANT: Yang, Jinping
; APPLICANT: Redin, William R.
; TITLE OF INVENTION: Stimulation Of Bone Growth With Thrombin
; TITLE OF INVENTION: Peptide Derivatives
; FILE REFERENCE: 3033.1002-001
; CURRENT APPLICATION NUMBER: US/09/909,122
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/219,300
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide fragment of Thrombin
; NAME/KEY: VARIANT
; LOCATION: (1)...(10)
; OTHER INFORMATION: Xaa at position two is Glu or Gln
; OTHER INFORMATION: Xaa at position nine is Phe, Met, Leu, His or Val
US-09-909-122-2
Query Match 78.0%; Score 46; DB 9; Length 10;
Best Local Similarity 80.0%; Pred. No. 0.62;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CEGDSGGPFV 10
| | | | |
Db 1 CXGDSGGPV 10

RESULT 7
US-10-050-692-2
; Sequence 2, Application US/10050692
; Publication No. US20020182205A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; APPLICANT: Crowther, Roger S.
; APPLICANT: Simmons, David J.
; APPLICANT: Yang, Jinping
; APPLICANT: Redin, William R.
; TITLE OF INVENTION: STIMULATION OF BONE GROWTH WITH THROMBIN
; TITLE OF INVENTION: PEPTIDE DERIVATIVES
; FILE REFERENCE: 3033.1002-004
; CURRENT APPLICATION NUMBER: US/10/050,692
; CURRENT FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: 09/909,122
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/219,300
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human fragment of prothrombin
; NAME/KEY: VARIANT
; LOCATION: (2)...(2)
; OTHER INFORMATION: Xaa = Glu or Gln

```

```

; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (9)...(9)
; OTHER INFORMATION: Xaa = Phe, Met, Leu, His or Val
US-10-050-692-2
Query Match 78.0%; Score 46; DB 13; Length 10;
Best Local Similarity 80.0%; Pred. No. 0.62;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CEGDSGGPFV 10
| | | | |
Db 1 CXGDSGGPV 10

RESULT 8
US-10-050-688-2
; Sequence 2, Application US/10050688
; Publication No. US20020198154A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; APPLICANT: Crowther, Roger S.
; APPLICANT: Stierberg, Janet
; APPLICANT: Bergmann, John
; TITLE OF INVENTION: STIMULATION OF CARTILAGE GROWTH WITH
; TITLE OF INVENTION: AGONISTS OF THE NON-PROTEOLYTICALLY ACTIVATED THROMBIN
; TITLE OF INVENTION: RECEPTOR
; FILE REFERENCE: 3033.1003-004
; CURRENT APPLICATION NUMBER: US/10/050,688
; CURRENT FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: 09/909,348
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/219,800
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide fragment of thrombin
; NAME/KEY: VARIANT
; LOCATION: (2)...(2)
; OTHER INFORMATION: Xaa = Glu or Gln
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (9)...(9)
; OTHER INFORMATION: Xaa = Phe, Met, Leu, His or Val
US-10-050-688-2
Query Match 78.0%; Score 46; DB 13; Length 10;
Best Local Similarity 80.0%; Pred. No. 0.62;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CEGDSGGPFV 10
| | | | |
Db 1 CXGDSGGPV 10

RESULT 9
US-09-572-404B-606
; Sequence 606, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0

```


SEQ ID NO 606
LENGTH: 10
TYPE: PRT
ORGANISM: Homo Sapiens
FEATURE:
OTHER INFORMATION: sequence located in C2 at 674-683 and may interact with Sequence
US-09-572-404B-606

Query Match 57.6%; Score 34; DB 10; Length 10;
Best Local Similarity 71.4%; Pred. No. 47;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CEGDSGG 7
|:|:|:|
DB 2 CKGESGG 8

RESULT 10

US-09-572-404B-3584
Sequence 3584, Application US/09572404B
Publication No. US20030078374A1
GENERAL INFORMATION:
APPLICANT: Proteom Ltd
TITLE OF INVENTION: Complementary peptide ligands from the human genome

FILE REFERENCE: Human patent
CURRENT APPLICATION NUMBER: US/09/572,404B
CURRENT FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 4203
SOFTWARE: ProtPatent version 1.0
SEQ ID NO 3584

LENGTH: 10
TYPE: PRT
ORGANISM: Homo Sapiens
FEATURE:
OTHER INFORMATION: sequence located in PXR1 OR PEX5 at 811-820 and may interact with
US-09-572-404B-3584

Query Match 47.5%; Score 28; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GDSGG 7
|:|:|:|
DB 6 GDSGG 10

RESULT 11

US-09-572-404B-3784
Sequence 3784, Application US/09572404B
Publication No. US20030078374A1
GENERAL INFORMATION:
APPLICANT: Proteom Ltd

TITLE OF INVENTION: Complementary peptide ligands from the human genome
FILE REFERENCE: Human patent
CURRENT APPLICATION NUMBER: US/09/572,404B
CURRENT FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 4203
SOFTWARE: ProtPatent version 1.0
SEQ ID NO 3784

LENGTH: 10
TYPE: PRT
ORGANISM: Homo Sapiens
FEATURE:
OTHER INFORMATION: sequence located in ERK5 OR ERK4 at 543-552 and may interact with
US-09-572-404B-3784

Query Match 45.8%; Score 27; DB 10; Length 10;
Best Local Similarity 83.3%; Pred. No. 5.8e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GDSGGP 8
|:|:|:|
DB 3 GASGGP 8

RESULT 12

US-09-572-404B-3785
Sequence 3785, Application US/09572404B
Publication No. US20030078374A1
GENERAL INFORMATION:
APPLICANT: Proteom Ltd

TITLE OF INVENTION: Complementary peptide ligands from the human genome
FILE REFERENCE: Human patent
CURRENT APPLICATION NUMBER: US/09/572,404B
CURRENT FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 4203
SOFTWARE: ProtPatent version 1.0
SEQ ID NO 3785

LENGTH: 10
TYPE: PRT
ORGANISM: Homo Sapiens
FEATURE:
OTHER INFORMATION: sequence located in ERK5 OR ERK4 at 543-552 and may interact with
US-09-572-404B-3785

Query Match 45.8%; Score 27; DB 10; Length 10;
Best Local Similarity 83.3%; Pred. No. 5.8e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GDSGGP 8
|:|:|:|
DB 3 GASGGP 8

RESULT 13

US-09-879-957-55
Sequence 55, Application US/09879957
Patent No. US20020034755A1
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.

HOFFMAN, No. US20020034755A1h
KAY, Brian K.
FOWLES, Dana M.
MCCONNELL, Stephen J.

TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
USING SAME

NUMBER OF SEQUENCES: 227
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP

STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA

ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/879,957

FILING DATE: 13-Jun-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,915

FILING DATE: 03-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Mistock, S. Leslie

REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-174
TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Other
LOCATION: 8
OTHER INFORMATION: Undefined
SEQUENCE DESCRIPTION: SEQ ID NO: 55:
US-09-879-957-55

Query Match 42.4%; Score 25; DB 9; Length 10;
Best Local Similarity 71.4%; Pred. No. 1.2e+03;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CEGDSGG 7
DB 1 CMGDSLG 7

RESULT 14
US-09-572-404B-51
; Sequence 51, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 51
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in CBFA2 OR AML1 at 360-369 and may interact with
; OTHER INFORMATION: Sequence 52 in this patent.
US-09-572-404B-51

Query Match 42.4%; Score 25; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGPF 9
DB 7 GGPF 10

RESULT 15
US-09-572-404B-53
; Sequence 53, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 53
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:

; OTHER INFORMATION: sequence located in CBFA2 OR AML1 at 360-369 and may interact with
; OTHER INFORMATION: Sequence 54 in this patent.
US-09-572-404B-53

Query Match 42.4%; Score 25; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGPF 9
DB 7 GGPF 10

Search completed: February 26, 2004, 09:31:59
Job time : 27.5 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 26, 2004, 09:19:44 ; Search time 15.5 Seconds
(without alignments)
33.307 Million cell updates/sec

Title: US-09-909-348-1

Perfect score: 59

Sequence: 1 CSGDSGGPVP 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 13857

Minimum DB seq length: 10

Maximum DB seq length: 10

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*

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3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*

4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*

5: /cgn2_6/ptodata/2/iaa/PGTUS_COMB.pep.*

6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	42.4	10	3	US-09-010-290-6
2	25	42.4	10	4	US-08-630-915A-55
3	24	40.7	10	1	US-08-282-758B-36
4	24	40.7	10	3	US-08-159-339A-827
5	24	40.7	10	3	US-08-139-802-58
6	24	40.7	10	4	US-08-659-786-58
7	24	40.7	10	4	US-08-407-620A-3
8	24	40.7	10	4	US-08-926-914-58
9	23	39.0	10	1	US-07-842-089E-15
10	23	39.0	10	1	US-08-264-485-15
11	23	39.0	10	1	US-08-340-428B-40
12	23	39.0	10	2	US-08-993-728A-9
13	23	39.0	10	2	US-08-362-864-36
14	23	39.0	10	2	US-08-902-367-7
15	23	39.0	10	3	US-08-535-170-9
16	23	39.0	10	3	US-08-836-786-2
17	23	39.0	10	3	US-08-713-354C-9
18	23	39.0	10	4	US-08-241-268-9
19	23	39.0	10	4	US-09-495-562-9
20	23	39.0	10	4	US-08-424-656-6
21	23	39.0	10	4	US-09-628-665-21
22	23	39.0	10	5	PCT-US93-07306-40
23	22.5	38.1	10	3	US-08-925-002-65
24	22.5	38.1	10	4	US-09-910-552-65
25	22	37.3	10	1	US-08-212-186A-3
26	22	37.3	10	1	US-08-105-222-6
27	22	37.3	10	1	US-08-435-238-2

Sequence 6, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 5, Appli
Sequence 897, App
Sequence 32, Appl
Sequence 81, Appl
Sequence 3, Appli
Sequence 9, Appli
Sequence 16, Appl
Sequence 18, Appl
Sequence 54, Appl
Sequence 16, Appl
Sequence 18, Appl
Sequence 32, Appl
Sequence 35, Appl
Sequence 18, Appl

ALIGNMENTS

RESULT 1
US-09-010-290-6
; Sequence 6, Application US/09010290
; Patent No. 6217846
; GENERAL INFORMATION:
; APPLICANT: Stuettle
; TITLE OF INVENTION: SYNTHETIC PEPTIDES FOR USE IN
; TITLE OF INVENTION: THROMBUS DETECTION
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff, Ltd.
; STREET: 28 State St., 28th Floor
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Wordperfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,290
; FILING DATE: 21-JAN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB8914020.6
; FILING DATE: 19-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB90/00933
; FILING DATE: 18-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/659,343
; FILING DATE: 21-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/963,127
; FILING DATE: 19-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/816,922
; FILING DATE: 12-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams, Ph.D., Kathleen A
; REGISTRATION NUMBER: 34,380
; REFERENCE/DOCKET NUMBER: 3998/73503
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-227-7111
; TELEFAX: 617-227-4399
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid

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; STRANDEDNESS: single
; TOPOLOGY: unknown
US-09-010-290-6

Query Match 42.4%; Score 25; DB 3; Length 10;
Best Local Similarity 80.0%; Pred. No. 5.3e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CEGDS 5
Db 5 CRGDS 9

RESULT 2
US-08-630-915A-55
; Sequence 55, Application US/08630915A
; Patent No. 6309820
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: HOFFMAN, No. 6309820h
; APPLICANT: KAY, Brian K.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: MCCONNELL, Stephen J.
; TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
; TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
; NUMBER OF SEQUENCES: 227
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/630,915A
; FILING DATE: 03-APR-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Miskock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-174
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNTE
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Other
; LOCATION: 8
; OTHER INFORMATION: Undefined
US-08-630-915A-55

Query Match 42.4%; Score 25; DB 4; Length 10;
Best Local Similarity 71.4%; Pred. No. 5.3e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CEGDSGG 7
Db 1 CMGDSLG 7

us-09-909-348-1.closed.ra1

RESULT 3
US-08-282-758B-36
; Sequence 36, Application US/08282758B
; Patent No. 5670310
; GENERAL INFORMATION:
; APPLICANT: Fields, Howard A.
; APPLICANT: Khudvakov, Yuri E.
; TITLE OF INVENTION: Methods and Compositions for
; TITLE OF INVENTION: Differential Diagnosis of Chronic and Acute Hepatitis C
; TITLE OF INVENTION: Virus Infection
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jones & Askew
; STREET: 191 Peachtree Street, 37th Floor
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: U.S.A.
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/282,758B
; FILING DATE: 29-JUL-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Green, Jamie L.
; REGISTRATION NUMBER: 32,467
; REFERENCE/DOCKET NUMBER: 03063-0100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 818-3700
; TELEFAX: (404) 818-3799
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-282-758B-36

Query Match 40.7%; Score 24; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 7.6e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 EGDSSG 7
Db 5 ESDAGG 10

us-08-282-758B-36

RESULT 4
US-08-159-339A-827
; Sequence 827, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; TITLE OF INVENTION: Uses
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 08-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 827:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
; US-08-159-339A-827

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Query Match 40.7%; Score 24; DB 3; Length 10;
Best Local Similarity 44.4%; Pred. No. 7.6e+02;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

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QY 2 EGDGGGPFV 10
DB 1 KGEAGAPGV 9

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RESULT 5
US-09-139-802-58
; Sequence 58, Application US/09139802
; Patent No. 6180084
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: NGR Receptor and Methods of Identifying Tumor Homing
; TITLE OF INVENTION: Molecules That Home to Angiogenic Vasculature Using
; TITLE OF INVENTION: Same
; FILE REFERENCE: P-LJ 3203
; CURRENT APPLICATION NUMBER: US/09/139,802
; CURRENT FILING DATE: 1998-08-25
; EARLIER APPLICATION NUMBER: 08/926,914
; EARLIER FILING DATE: 1997-09-10
; EARLIER APPLICATION NUMBER: 08/710,067
; EARLIER FILING DATE: 1996-09-10
; NUMBER OF SEQ ID NOS: 226
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 58
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; US-09-139-802-58

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Query Match 40.7%; Score 24; DB 3; Length 10;
Best Local Similarity 66.7%; Pred. No. 7.6e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY 1 CEGDSG 6
DB 1 CEGVNG 6

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RESULT 6
US-09-659-786-58
; Sequence 58, Application US/09659786
; Patent No. 6491894
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: NGR Receptor and Methods of Identifying Tumor Homing
; TITLE OF INVENTION: Molecules That Home to Angiogenic Vasculature Using
; TITLE OF INVENTION: Same
; FILE REFERENCE: P-LJ 3203
; CURRENT APPLICATION NUMBER: US/09/659,786
; CURRENT FILING DATE: 2000-09-11
; PRIOR APPLICATION NUMBER: 08/926,914
; PRIOR FILING DATE: 1997-09-10
; PRIOR APPLICATION NUMBER: 08/710,067
; PRIOR FILING DATE: 1996-09-10
; NUMBER OF SEQ ID NOS: 226
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 58
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; US-09-659-786-58

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Query Match 40.7%; Score 24; DB 4; Length 10;
Best Local Similarity 66.7%; Pred. No. 7.6e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY 1 CEGDSG 6
DB 1 CEGVNG 6

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RESULT 7
US-08-407-620A-3
; Sequence 3, Application US/08407620A
; Patent No. 6569430
; GENERAL INFORMATION:
; APPLICANT: WALDMANN, HERMAN
; APPLICANT: CLARK, MICHAEL R.
; APPLICANT: WINTER, GREGORY P.
; APPLICANT: RIECHMANN, LUTZ
; TITLE OF INVENTION: ANTIBODIES
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/407,620A
; FILING DATE: 21-MAR-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/235,705
; FILING DATE: 29-APR-1994

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/099,480
; FILING DATE: 30-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/921,601
; FILING DATE: 03-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/424,233
; FILING DATE: 12-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 88036228
; FILING DATE: 12-FEB-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 8804464
; FILING DATE: 25-FEB-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: MITCHARD, LEONARD C.
; REGISTRATION NUMBER: 29,009
; REFERENCE/DOCKET NUMBER: 604-325
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; TELEX: 200797 NIXN UR
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-407-620A-3

Query Match 40.7%; Score 24; DB 4; Length 10;
Best Local Similarity 50.0%; Pred. No. 7.6e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 EGDGGPF 9
DB 1 EGHTRAPP 8

RESULT 8
US-08-926-914-58
; Sequence 58, Application US/08926914
; Patent No. 6576239
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; TITLE OF INVENTION: Tumor Homing Molecules, Conjugates
; TITLE OF INVENTION: Derived Therefrom, and Methods of Using Same
; NUMBER OF SEQUENCES: 199
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/926,914
; FILING DATE: 10-SEP-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 2725
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949

;
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: both
; MOLECULE TYPE: peptide
; US-08-926-914-58

Query Match 40.7%; Score 24; DB 4; Length 10;
Best Local Similarity 66.7%; Pred. No. 7.6e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CEGDSG 6
DB 1 CEGVNG 6

RESULT 9
US-07-842-089E-15
; Sequence 15, Application US/07842089E
; Patent No. 5356875
; GENERAL INFORMATION:
; APPLICANT: SARMIENTOS, PAOLO
; APPLICANT: DE Taxis DU POET, PHILIPPE
; APPLICANT: NITTI, GIAMPAOLO
; APPLICANT: SCACHERI, EMANUELA
; TITLE OF INVENTION: ANTI-THROMBIN POLYPEPTIDES
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 Jefferson Davis Highway, Fourth Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/842,089E
; FILING DATE: 26-FEB-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5356875man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 769-265-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 412-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Hirudinaria manillensis
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..10
; OTHER INFORMATION: /note= "This sequence corresponds
; OTHER INFORMATION: to amino acids 27-36 of SEQ ID NO:1."
; US-07-842-089E-15

Query Match 39.0%; Score 23; DB 1; Length 10;
Best Local Similarity 57.1%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CEGDSGG 7
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Db 2 CEMDGG 8

RESULT 10
US-08-264-485-15
; Sequence 15, Application US/08264485
; Patent No. 5439820
; GENERAL INFORMATION:
; APPLICANT: SARMIENTOS, PAOLO
; APPLICANT: DE Taxis DU POET, PHILIPPE
; APPLICANT: NITTI, GIAMPAOLO
; APPLICANT: SCACHERI, EMANUELA
; TITLE OF INVENTION: ANTI-THROMBIN POLYPEPTIDES
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
; ADDRESS: P.C.
; STREET: 1755 Jefferson Davis Highway, Fourth Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/264,485
; FILING DATE: 23-JUN-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/842,089
; FILING DATE: 26-FEB-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, No. 5439820man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 769-265-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 412-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Hirudinaria manillensis
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..10
; OTHER INFORMATION: /note= "This sequence corresponds
; to amino acids 27-36 of SEQ ID NO:1."
US-08-264-485-15
Query Match 39.0%; Score 23; DB 1; Length 10;
Best Local Similarity 57.1%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 CEGDSGG 7
Db 2 CEMDGG 8

RESULT 11
US-08-340-428B-40
; Sequence 40, Application US/08340428B
; Patent No. 5648465
; GENERAL INFORMATION:
; APPLICANT: MARGOLIS, Richard U.
; APPLICANT: RAUCH, Uwe
; APPLICANT: MARGOLIS, Renee K.
; TITLE OF INVENTION: CLONING, EXPRESSION AND USES FOR A
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/340,428B
; FILING DATE: 14 No. 5648465ember 1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/922,911
; FILING DATE: 03 August 1992
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Browdy, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: Margolis-1a
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-340-428B-40
Query Match 39.0%; Score 23; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3 GDSGGP 8
Db 3 GDQGTP 8

RESULT 12
US-08-993-738A-9
; Sequence 9, Application US/08993738A
; Patent No. 5928938
; GENERAL INFORMATION:
; APPLICANT: van der Bruggen, Pierre; DePlaeen Etienne;
; APPLICANT: Boon-Fallieur, Thierry
; TITLE OF INVENTION: Isolated Peptides Which Complex With
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski L.L.P.
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect


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; OTHER INFORMATION: /label= D-Tyr
; OTHER INFORMATION: /note= "The tyrosine residue is in the D-stereo-
; OTHER INFORMATION: chemical configuration"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1.5
; OTHER INFORMATION: /label= Cyclic
; OTHER INFORMATION: /note= "The sidechain sulfur of the Cys
; OTHER INFORMATION: residue is covalently linked to the amino
; OTHER INFORMATION: terminus by a -CH2CO- group."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 8.10
; OTHER INFORMATION: /label= Tc-99m-chelator
; OTHER INFORMATION: /note= "The sidechain sulfur atoms of both Cys
; OTHER INFORMATION: residues are each protected with an
; OTHER INFORMATION: acetamidomethyl group"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 10
; OTHER INFORMATION: /label= Amide
; OTHER INFORMATION: /note= "The carboxyl terminus is modified to an
; OTHER INFORMATION: amide"
; US-08-902-367-7
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; Query Match
; Best Local Similarity 39.0%; Score 23; DB 2; Length 10;
; Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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; QY 3 GDSGG 7
; DB 3 GDCGG 7
;
; RESULT 15
; US-08-535-170-9
; Sequence 9, Application US/08535170
; Patent No. 6056940
; GENERAL INFORMATION:
; APPLICANT: Dean, Richard T.
; APPLICANT: Lister-James, John
; APPLICANT: Civitello, Edgar R.
; TITLE OF INVENTION: Radiolabeled Compounds for Thrombus
; TITLE OF INVENTION: Imaging
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/535,170
; FILING DATE: 11-JAN-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6056940nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 90,1104-KK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312 913 0001
; TELEFAX: 312 913 0002
; TELEX:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
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; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /label= D-Tyr
; OTHER INFORMATION: /note= "The tyrosine residue is in the D-stereo-
; OTHER INFORMATION: chemical configuration"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1.5
; OTHER INFORMATION: /label= Cyclic
; OTHER INFORMATION: /note= "The sidechain sulfur of the Cys
; OTHER INFORMATION: residue is covalently linked to the amino
; OTHER INFORMATION: terminus by a -CH2CO- group."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 8.10
; OTHER INFORMATION: /label= Tc-99m-chelator
; OTHER INFORMATION: /note= "The sidechain sulfur atoms of both Cys
; OTHER INFORMATION: residues are each protected with an
; OTHER INFORMATION: acetamidomethyl group"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 10
; OTHER INFORMATION: /label= Amide
; OTHER INFORMATION: /note= "The carboxyl terminus is modified to an
; OTHER INFORMATION: amide"
; US-08-535-170-9
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Query Match 39.0%; Score 23; DB 3; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 3 GDSGG 7
DB 3 GDCGG 7
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Search completed: February 26, 2004, 09:24:49
Job time : 17.5 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 26, 2004, 09:17:19 ; Search time 13.5 Seconds
(without alignments)
71.253 Million cell updates/sec

Title: US-09-909-348-2

Perfect score: 50

Sequence: 1 CXGDSGGPXV 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 311

Minimum DB seq length: 10

Maximum DB seq length: 10

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 78.*

1: Piri:*

2: Piri:*

3: Piri:*

4: Piri:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	20	40.0	10	2 PH0944	T-cell receptor be
3	18	36.0	10	2 C39572	sperm-activating p
4	18	36.0	10	2 B60589	sperm-activating p
5	17	34.0	10	2 D60527	sperm-activating p
6	17	34.0	10	2 XGHUE	erythrocyte membra
7	17	34.0	10	2 PT0632	T-cell receptor be
8	17	34.0	10	2 PT0664	T-cell receptor be
9	17	34.0	10	2 PH0927	T-cell receptor be
10	16	32.0	10	1 XASNFC	angiotensin-conver
11	16	32.0	10	2 F60787	sperm-activating p
12	16	32.0	10	2 E39572	sperm-activating p
13	16	32.0	10	2 F60589	sperm-activating p
14	16	32.0	10	2 D60589	sperm-activating p
15	16	32.0	10	2 B60589	sperm-activating p
16	16	32.0	10	2 A60588	sperm-activating p
17	16	32.0	10	2 PT0243	Ig heavy chain CRD
18	16	32.0	10	2 PT0215	T-cell receptor be
19	16	32.0	10	2 PH0900	T-cell receptor be
20	15	30.0	10	1 ECLQIM	tachykinin I - mig
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25	14	28.0	10	2 PT0084	protein QA600021 -
26	14	28.0	10	2 B56899	serum heterodimer,
27	14	28.0	10	2 PX0060	lysosome-associa
28	14	28.0	10	2 A32195	Na+/K+-exchangin
29	13	26.0	10	2 S65388	Cytochrome-c oxida

30	13	26.0	10	2 C45474	thrombospondin 2 -
31	13	26.0	10	2 B33710	ornithine decarbox
32	13	26.0	10	2 H60787	sperm-activating p
33	13	26.0	10	2 B60788	sperm-activating p
34	13	26.0	10	2 C60788	sperm-activating p
35	13	26.0	10	2 D60788	sperm-activating p
36	13	26.0	10	2 D60787	sperm-activating p
37	13	26.0	10	2 C60787	sperm-activating p
38	13	26.0	10	2 A60787	sperm-activating p
39	13	26.0	10	2 B60787	sperm-activating p
40	13	26.0	10	2 A60788	sperm-activating p
41	13	26.0	10	2 A60527	sperm-activating p
42	13	26.0	10	2 G60527	sperm-activating p
43	13	26.0	10	2 B60527	sperm-activating p
44	13	26.0	10	2 C60527	sperm-activating p
45	13	26.0	10	2 C60589	sperm-activating p

ALIGNMENTS

RESULT 1

PH0925

T-cell receptor beta chain V-D-J region (isolate 11) - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)

C>Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997

C:Accession: PH0925

R:Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.

J. Exp. Med. 174, 1467-1476, 1991

A>Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic A.Reference number: PH0891; MUID:92078857; PMID:1836012

A:Accession: PH0925

A:Molecule type: mRNA

A:Residues: 1-10 <GOL>

A:Experimental source: concanavalin A-activated lymphoblast

C:Keywords: T-cell receptor

Query Match 42.0%; Score 21; DB 2; Length 10;

Best Local Similarity 42.9%; Pred. No. 8.8e+02;

Matches 3; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CXGDSGG 7

DB 1 CASSDGG 7

RESULT 2

PH0944

T-cell receptor beta chain V-D-J region (clone 15) - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)

C>Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997

C:Accession: PH0944

R:Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.

J. Exp. Med. 174, 1467-1476, 1991

A>Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic A.Reference number: PH0891; MUID:92078857; PMID:1836012

A:Accession: PH0944

A:Molecule type: mRNA

A:Residues: 1-10 <GOL>

A:Experimental source: complete Freund's adjuvant-immunized lymph node

A>Note: the authors translated the codon GAC for residue 9 as Glu

C:Keywords: T-cell receptor

Query Match 40.0%; Score 20; DB 2; Length 10;

Best Local Similarity 42.9%; Pred. No. 1.3e+03;

Matches 3; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CXGDSGG 7

DB 1 CASSPGG 7

RESULT 3

C39572
 sperm-activating peptide TG-3 - sea urchin (Tripneustes gratilla)
 N:Alternate names: speract homolog TG-3
 C:Species: Tripneustes gratilla
 C:Date: 10-Jul-1992 #sequence_revision 10-Jul-1992 #text_change 18-Aug-2000
 C:Accession: C39572
 R:Yoshino, K.; Takao, T.; Suhara, M.; Kitai, T.; Hori, H.; Nomura, K.; Yamaguchi, M.; Sh
 Biochemistry 30, 6203-6209, 1991
 A:Title: Identification of a novel amino acid, o-bromo-L-phenylalanine, in egg-associate
 A:Reference number: A39572; MUID:91283461; PMID:2059627
 A:Accession: C39572
 A:Molecule type: protein
 A:Residues: 1-10 <YOS>
 C:Superfamily: unassigned animal peptides
 C:Keywords: bromine
 F:2/Modified site: 2'-bromophenylalanine (Phe) #status experimental

Query Match 36.0%; Score 18; DB 2; Length 10;
 Best Local Similarity 75.0%; Pred. No. 3.1e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 4 DSGG 7
 DB 5 DGGG 8

RESULT 4
 B60589
 sperm-activating peptide (Gly-3, Ser-5, Ile-9 SAP-I) - slate-pencil urchin (Heterocentrotus
 C:Species: Heterocentrotus mamillatus
 C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Aug-2000
 C:Accession: B60589
 R:Yoshino, K.I.; Kajijura, H.; Nomura, K.; Takao, T.; Shimonishi, Y.; Kurita, M.; Yamaguchi
 Comp. Biochem. Physiol. B 94, 739-751, 1989
 A:Title: A halogenated amino acid-containing sperm activating peptide and its related pe
 otus nudus, Echinometra mathaei and Heterocentrotus mamillatus.
 A:Reference number: A60527
 A:Accession: B60589
 A:Molecule type: protein
 A:Residues: 1-10 <YOS>
 C:Superfamily: unassigned animal peptides

Query Match 36.0%; Score 18; DB 2; Length 10;
 Best Local Similarity 80.0%; Pred. No. 3.1e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 3 GDSGG 7
 DB 3 GLSGG 7

RESULT 5
 D60527
 sperm-activating peptide (Gly-5 SAP-I) - sea urchin (Tripneustes gratilla)
 N:Alternate names: speract homolog TG-6
 C:Species: Tripneustes gratilla
 C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Aug-2000
 C:Accession: D60527; F39572
 R:Yoshino, K.I.; Kajijura, H.; Nomura, K.; Takao, T.; Shimonishi, Y.; Kurita, M.; Yamaguchi
 Comp. Biochem. Physiol. B 94, 739-751, 1989
 A:Title: A halogenated amino acid-containing sperm activating peptide and its related pe
 otus nudus, Echinometra mathaei and Heterocentrotus mamillatus.
 A:Reference number: A60527
 A:Accession: D60527
 A:Molecule type: protein
 A:Residues: 1-10 <YOS>
 A:Note: this peptide did not contain bromophenylalanine
 R:Yoshino, K.; Takao, T.; Suhara, M.; Kitai, T.; Hori, H.; Nomura, K.; Yamaguchi, M.; Sh
 Biochemistry 30, 6203-6209, 1991
 A:Title: Identification of a novel amino acid, o-bromo-L-phenylalanine, in egg-associate
 A:Reference number: A39572; MUID:91283461; PMID:2059627
 A:Accession: F39572
 A:Molecule type: protein

A:Residues: 1-10 <YOS>
 A:Note: this peptide contained bromophenylalanine
 C:Superfamily: unassigned animal peptides
 C:Keywords: bromine
 F:2/Modified site: 2'-bromophenylalanine (Phe) (partial) #status experimental

Query Match 34.0%; Score 17; DB 2; Length 10;
 Best Local Similarity 57.1%; Pred. No. 4.6e+03;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 4 DSGGPXV 10
 DB 3 DLGGGV 9

RESULT 6
 XGHUE
 erythrocyte membrane glycopeptide - human
 C:Species: Homo sapiens (man)
 C:Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000
 C:Accession: A03187
 R:Weiss, J.B.; Lote, C.J.; Bobinski, H.
 Nature New Biol. 234, 25-26, 1971
 A:Title: New low molecular weight glycopeptide containing triglycosylcysteine in human e
 A:Reference number: A03187; MUID:72034940; PMID:5286858
 A:Accession: A03187
 A:Molecule type: protein
 A:Residues: 1-10 <WEI>
 C:Comment: The identity of the glycoprotein from which this peptide is derived is unknown
 found (see PIR:XGHUEU).
 C:Superfamily: unassigned animal peptides
 C:Keywords: Glycoprotein
 F:1/Binding site: carbohydrate (Cys) (covalent) #status experimental

Query Match 34.0%; Score 17; DB 2; Length 10;
 Best Local Similarity 60.0%; Pred. No. 4.6e+03;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 CXGDS 5
 DB 1 CEGHS 5

RESULT 7
 PT0632
 T-cell receptor beta chain V-D-J region (120-1A) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C:Accession: PT0632
 R:Feeney, A.J.
 J. Exp. Med. 174, 115-124, 1991
 A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
 A:Reference number: PT0509; MUID:91277601; PMID:1711558
 A:Accession: PT0632
 A:Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-10 <PEE>
 A:Experimental source: newborn thymus, strain BALB/c
 C:Keywords: T-cell receptor

Query Match 34.0%; Score 17; DB 2; Length 10;
 Best Local Similarity 60.0%; Pred. No. 4.6e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 3 GDSGG 7
 DB 3 GDAPG 7

RESULT 8
 PT0664
 T-cell receptor beta chain V-D-J region (121-2L) - mouse (fragment)
 C:Species: Mus musculus (house mouse)

C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C;Accession: PT0664

C;Feeney, A.J. 174, 115-124, 1991

A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A;Reference number: PT0509; MUID:91277601; PMID:1711558

A;Accession: PT0664

A;Status: translation not shown

A;Molecule type: mRNA

A;Residues: 1-10 <FE>

A;Experimental source: day 4 postnatal thymus, strain BALB/c

C;Keywords: T-cell receptor

Query Match 34.0%; Score 17; DB 2; Length 10;

Best Local Similarity 60.0%; Pred. No. 4.6e+03;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GDSGG 7

Db 3 GDTPE 7

RESULT 9

PH0927

T-cell receptor beta chain V-D-J region (clone 13) - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997

C;Accession: PH0927

R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.

J. Exp. Med. 174, 1467-1476, 1991

A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic

A;Reference number: PH0891; MUID:92078857; PMID:1836012

A;Accession: PH0927

A;Molecule type: mRNA

A;Residues: 1-10 <GO>

A;Experimental source: concanavalin A-activated lymphoblast

C;Keywords: T-cell receptor

Query Match 34.0%; Score 17; DB 2; Length 10;

Best Local Similarity 75.0%; Pred. No. 4.6e+03;

Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 SGGP 8

Db 4 SAGP 7

RESULT 10

XASNFC

angiotensin-converting enzyme inhibitor - aspiv viper

C;Species: Vipera aspis (aspiv viper)

C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 08-Dec-1995

C;Accession: A60377

R;Komori, Y.; Sugihara, H.

Int. J. Biochem. 22, 767-771, 1990

A;Title: Characterization of a new inhibitor for angiotensin converting enzyme from the

A;Reference number: A60377; MUID:90382616; PMID:2169439

A;Accession: A60377

A;Molecule type: protein

A;Residues: 1-10 <KM>

C;Superfamily: bradykinin-potentiating peptide

C;Keywords: angiotensin-converting enzyme inhibitor; pyroglutamic acid

F1/Modified site: Pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 32.0%; Score 16; DB 1; Length 10;

Best Local Similarity 75.0%; Pred. No. 7e+03;

Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GPXV 10

Db 5 GPXV 8

RESULT 11

F60787

sperm-activating peptide (Ser-5 speract) - sea urchin (Anthocidaris crassispina)

C;Species: Anthocidaris crassispina

C;Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 18-Aug-2000

C;Accession: F60787

R;Suzuki, N.; Kajiyura, H.; Nomura, K.; Garbers, D.L.; Yoshino, K.; Kurita, M.; Tanaka, H.

Comp. Biochem. Physiol. B 99, 687-693, 1988

A;Title: Some more speract derivatives associated with eggs of sea urchins, Pseudocentrotus

A;Reference number: A60787; MUID:88242184; PMID:3378407

A;Accession: F60787

A;Molecule type: protein

A;Residues: 1-10 <SU>

C;Comment: This oligopeptide from egg jelly is one of several from this species, all of v

at shows some, but not absolute, species restriction.

C;Superfamily: unassigned animal peptides

Query Match 32.0%; Score 16; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 7e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 SGG 7

Db 5 SGG 7

RESULT 12

E39572

sperm-activating peptide TG-5 - sea urchin (Tripneustes gratilla)

N;Alternate names: speract homolog TG-5

C;Species: Tripneustes gratilla

C;Date: 10-Jul-1992 #sequence_revision 10-Jul-1992 #text_change 18-Aug-2000

C;Accession: E39572

R;Yoshino, K.; Takao, T.; Suhrara, M.; Kitai, T.; Hori, H.; Nomura, K.; Yamaguchi, M.; Shi

Biochemistry 30, 6203-6209, 1991

A;Title: Identification of a novel amino acid, O-bromo-L-phenylalanine, in egg-associated

A;Reference number: A39572; MUID:91283461; PMID:2059627

A;Accession: E39572

A;Molecule type: protein

A;Residues: 1-10 <YO>

C;Superfamily: unassigned animal peptides

C;Keywords: bromine

F1/Modified site: 2'-bromophenylalanine (Phe) #status experimental

Query Match 32.0%; Score 16; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 7e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 SGG 7

Db 5 SGG 7

RESULT 13

F60589

sperm-activating peptide (Asn-3, Ser-5 SAP-I) - Echinometra mathaei (type A)

C;Species: Echinometra mathaei

C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Aug-2000

C;Accession: F60589

R;Yoshino, K.; Kajiyura, H.; Nomura, K.; Takao, T.; Shimonishi, Y.; Kurita, M.; Yamaguchi

Comp. Biochem. Physiol. B 94, 739-751, 1989

A;Title: A halogenated amino acid-containing sperm activating peptide and its related pe

ctus nudus, Echinometra mathaei and Heterocentrotus mammillatus.

A;Reference number: A60527

A;Accession: F60589

A;Molecule type: protein

A;Residues: 1-10 <YO>

C;Superfamily: unassigned animal peptides

Query Match 32.0%; Score 16; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 7e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GPXV 10

Db 5 GPXV 8

QY 5 SGG 7
 |||
 Db 5 SGG 7

RESULT 14

D60589
 sperm-activating peptide (Ser-3,5 SAP-I) - Echinometra mathaei
 C:Species: Echinometra mathaei
 C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Aug-2000
 C:Accession: D60589
 R:Yoshino, K.I.; Kajiura, H.; Nomura, K.; Takao, T.; Shimonishi, Y.; Kurita, M.; Yamaguchi, T.
 Comp. Biochem. Physiol. B 94, 739-751, 1989
 A:Title: A halogenated amino acid-containing sperm activating peptide and its related peptides
 A:Reference number: A60527
 A:Accession: D60589
 A:Molecule type: protein
 A:Residues: 1-10 <YOS>
 A>Note: an identical peptide was isolated from Echinometra mathaei type A and type B
 C:Superfamily: unassigned animal peptides

Query Match 32.0%; Score 16; DS 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 SGG 7
 |||
 Db 5 SGG 7

RESULT 15

E60589
 sperm-activating peptide (Tyr-2, Ser-3,5, Ala-8, Asp-10 SAP-I) - Echinometra mathaei
 C:Species: Echinometra mathaei
 C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Aug-2000
 C:Accession: E60589
 R:Yoshino, K.I.; Kajiura, H.; Nomura, K.; Takao, T.; Shimonishi, Y.; Kurita, M.; Yamaguchi, T.
 Comp. Biochem. Physiol. B 94, 739-751, 1989
 A:Title: A halogenated amino acid-containing sperm activating peptide and its related peptides
 A:Reference number: A60527
 A:Accession: E60589
 A:Molecule type: protein
 A:Residues: 1-10 <YOS>
 A>Note: an identical peptide was isolated from Echinometra mathaei type A and type B
 C:Superfamily: unassigned animal peptides

Query Match 32.0%; Score 16; DS 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 SGG 7
 |||
 Db 5 SGG 7

Search completed: February 26, 2004, 09:24:05
 Job time: 13.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 26, 2004, 09:02:09 ; Search time 10.5 Seconds
(without alignments)
49.591 Million cell updates/sec

Title: US-09-909-348-2

Perfect score: 50

Sequence: 1 CXGDSGGPXV 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 120

Minimum DB seq length: 10

Maximum DB seq length: 10

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	17	34.0	10	1 GLEM_HUMAN	P02728 homo sapien
2	16	32.0	10	1 BPP_VIPAS	P31351 vipera aspi
3	16	32.0	10	1 ESTA_SCHGA	P81012 schizaphis
4	15	30.0	10	1 COXQ_RABIT	P80336 cryotolagus
5	14	28.0	10	1 FAR6_PANRE	P82660 panagrellus
6	14	28.0	10	1 TRP8_LEUMA	P81740 leucophaea
7	13	26.0	10	1 COXO_RAT	P80432 rattus norv
8	13	26.0	10	1 COXO_THUOB	P80982 thunnus obe
9	13	26.0	10	1 PNEU_HUMAN	P22103 homo sapien
10	13	26.0	10	1 PNEU_RAT	P21996 rattus norv
11	13	26.0	10	1 TKS2_AEDAE	P42535 aedes aegyp
12	12	24.0	10	1 COXH_ONCMY	P80331 oncorhynchu
13	12	24.0	10	1 CU30_LOCOMI	P11735 locusta mig
14	12	24.0	10	1 FAR7_MACRS	P83280 macrobrachi
15	12	24.0	10	1 FARP_MYTED	P42560 mytilus edu
16	12	24.0	10	1 TKS1_AEDAE	P42634 aedes aegyp
17	12	24.0	10	1 TPIS_NICPL	P19118 nicotiana p
18	12	24.0	10	1 UPAS_HUMAN	P30094 homo sapien
19	10	20.0	10	1 CATB_SHEEP	P83205 ovis aries
20	10	20.0	10	1 FARP_LOCOMI	P38553 locusta mig
21	10	20.0	10	1 GAJU_HUMAN	P01358 homo sapien
22	10	20.0	10	1 GONI_CLUPA	P81749 clupea pall
23	10	20.0	10	1 HTP_HELZE	P16353 heliothis z
24	10	20.0	10	1 LSK2_LEUMA	P09039 leucophaea
25	10	20.0	10	1 MOSQ_CLYJA	P19982 clypeaster
26	10	20.0	10	1 NS1_MYCTU	P81135 mycobacteri
27	10	20.0	10	1 PVK_LOCOMI	P83382 locusta mig
28	10	20.0	10	1 RRPL_PHODV	P35946 phocine dis
29	10	20.0	10	1 SLAP_BACTG	P49325 bacillus th
30	10	20.0	10	1 TKL2_LOCOMI	P6224 locusta mig
31	10	20.0	10	1 TKNE_CHICK	P19851 gallus gall
32	10	20.0	10	1 TKNB_RANCA	P22689 rana catesb
33	10	20.0	10	1 TKNB_RANRI	P29135 rana ridibu

34	10	20.0	10	1 TMOF_AEDAE	P19425 aedes aegyp
35	10	20.0	10	1 TR27_LEUMA	P81739 leucophaea
36	10	20.0	10	1 UH05_RAT	P56573 rattus norv
37	10	20.0	10	1 UHA3_HUMAN	P40930 homo sapien
38	10	20.0	10	1 UPAS_HUMAN	P30091 homo sapien
39	10	20.0	10	1 URE3_MORMO	P17339 morganella
40	9	18.0	10	1 BPP2_BOTIN	P30422 bothriops in
41	9	18.0	10	1 BPP2_BOTJA	P01022 bothriops in
42	9	18.0	10	1 BPP8_BOTIN	P30426 bothriops in
43	9	18.0	10	1 GON2_CHEPR	P80678 chelyosoma
44	9	18.0	10	1 PAPI_PARMA	P81963 pardachirus
45	9	18.0	10	1 PPCK_FASHE	P80825 fasciola he

ALIGNMENTS

RESULT 1
ID GLEM_HUMAN STANDARD; PRT; 10 AA.
AC P02728:
21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Erythrocyte membrane glycopeptide.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=72034940; PubMed=5286859;
RA Weiss J.B., Lote C.J., Bobinski H.;
RT "New low molecular weight glycopeptide containing triglucoylcysteine in human erythrocyte membrane.";
RL Nature New Biol. 234:25-26(1971).
CC -!- PTM: S-linked glycan consists of Glc-Glc-Glc trisaccharide.
CC -!- MISCELLANEOUS: The identity of the glycoprotein from which this peptide is derived is unknown. No physiological function has been attributed.
CC PIR; A03187; XGHUE.
DR Glycoprotein; Erythrocyte.
KW CARBOHYD 1
FT S-LINKED (GLC...);
SQ SEQUENCE 10 AA; 1049 MW; 239BFEEA1F5B1E8 CRC64;
Query Match 34.0%; Score 17; DB 1; Length 10;
Best Local Similarity 60.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CXGDS 5
Db 1 CEGHS 5

RESULT 2

ID BPP_VIPAS STANDARD; PRT; 10 AA.
AC P31351:
01-JUL-1993 (Rel. 26, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide (Angiotensin-converting enzyme inhibitor).
OS Vipera aspis (Aspic viper).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Viperinae; Vipera.
CX NCBI_TaxID=8706;
RN [1]
RP SEQUENCE.
RX TISSUE=Venom;
RX MEDLINE=90382616; PubMed=2169439;
RX Komori Y., Sugihara H.;

```
RT "Characterization of a new inhibitor for angiotensin converting
RT enzyme from the venom of Vipera aspis aspis."
RT Int. J. Biochem. 22:767-771(1990).
CC -!- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
CC PIR: A60377; XASNPC.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 10 AA; 1062 MW; 3BA827C327686773 CRC64;

Query Match 32.0%; Score 16; DB 1; Length 10;
Best Local Similarity 75.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GPXV 10
DB 5 GPKV 8

RESULT 3
ESTA SCHGA STANDARD; PRT; 10 AA.
ID -ESTA SCHGA STANDARD; PRT; 10 AA.
AC P81012;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Esterase 52 kDa subunit (EC 3.1.1.1) (Carboxylic-ester hydrolase)
DE (Fragment).
DE Schizaphis graminum (Aphid).
OS Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
OC Aphidoidea; Aphididae; Aphidini; Schizaphis.
OX NCBI_TaxID=13262;
RN [1]
SQ SEQUENCE.
RX MEDLINE=97468499; PubMed=9327586;
RA Siegfried B.D., Ono M., Swanson J.J.;
RT "Purification and characterization of a carboxylesterase associated
RT with organophosphate resistance in the greenbug, Schizaphis graminum
RT (Homoptera: Aphididae).";
RT Arch. Insect Biochem. Physiol. 36:229-240(1997).
CC -!- CATALYTIC ACTIVITY: A carboxylic ester + H(2)O = an alcohol + a
CC carboxylic anion.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC InterPro: IPR002018; CarbesteraseB.
DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; PARTIAL.
DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; PARTIAL.
KW Hydrolase; Serine esterase.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1025 MW; 018ABE587865A2C0 CRC64;

Query Match 32.0%; Score 16; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 SGG 7
DB 5 SGG 7

RESULT 4
COXQ RABIT STANDARD; PRT; 10 AA.
ID COXQ RABIT STANDARD; PRT; 10 AA.
AC P80336;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytochrome c oxidase polypeptide VIII-liver/heart (EC 1.9.3.1)
DE (Fragment).
DE COX8H.
GN COX8H.

OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
SQ SEQUENCE.
RP TISSUE=Heart, and Liver;
RA Freund R., Kadenbach B.;
RL Submitted (MAR-1994) to Swiss-Prot.
CC -!- FUNCTION: This protein is one of the nuclear-coded polypeptide
CC chains of cytochrome c oxidase, the terminal oxidase in
CC mitochondrial electron transport.
CC -!- CATALYTIC ACTIVITY: 4 ferrocyanochrome c + O(2) = 4 ferricytochrome
CC c + 2 H(2)O.
CC -!- SIMILARITY: Belongs to the cytochrome c oxidase VIII family.
CC Oxidoreductase; Mitochondrion.
KW NON_TER 10 10
FT MOD RES 10 10
SQ SEQUENCE 10 AA; 1027 MW; 2C325CB40DC76338 CRC64;

Query Match 30.0%; Score 15; DB 1; Length 10;
Best Local Similarity 75.0%; Pred. No. 3.2e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 SGGP 8
DB 2 SGGP 5

RESULT 5
FAR6 PANRE STANDARD; PRT; 10 AA.
ID -FAR6 PANRE STANDARD; PRT; 10 AA.
AC P83650;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE FMRamide-like neuropeptide PF6 (NGAPQPFVRF-amide).
DE Panagrellus redivivus.
OS Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
OC Panagrolaimoidea; Panagrolaimidae; Panagrellus.
OX NCBI_TaxID=6233;
RN [1]
SQ SEQUENCE, FUNCTION, AND AMIDATION.
RA Moffett C.L., Marks N.J., Halton D.W., Thomson D.P., Geary T.G.,
RA Maule A.G.;
RT "Isolation, characterization and pharmacology of FMRamide-related
RT peptides (Farps) from free-living nematode, Panagrellus redivivus.";
RL Submitted (JUL-2000) to Swiss-Prot.
CC -!- FUNCTION: Myoactive.
CC -!- SIMILARITY: Belongs to the FARP (FMRamide related peptide)
CC family.
CC Neuropeptide; Amidation.
KW MOD RES 10 10
FT MOD RES 10 10
SQ SEQUENCE 10 AA; 1132 MW; CB13E4C9D776C76D CRC64;

Query Match 28.0%; Score 14; DB 1; Length 10;
Best Local Similarity 50.0%; Pred. No. 4.9e+03;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 SGGP 8
DB 1 NGAP 4

RESULT 6
TRP8 LEUMA STANDARD; PRT; 10 AA.
ID -TRP8 LEUMA STANDARD; PRT; 10 AA.
AC P81740;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tachykinin-related peptide 8 (LemRP 8).
DE Leucophaea maderae (Madeira cockroach).
OS Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
```

OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
 OC Blaberidae; Leucophaea.
 OX NCBI_TaxID=6988;

RN [1] SEQUENCE, AND MASS SPECTROMETRY.

RP TISSUE=Brain;

RC MEDLINE=97269266; PubMed=9114447;

RX Muren J.E., Naessel D.R.;

RA "Seven tachykinin-related peptides isolated from the brain of the
 RT Madeira cockroach; evidence for tissue-specific expression of
 RT isoforms.";

RT Peptides 18:7-15(1997).

RL CC -!- FUNCTION: Myoactive peptide. Increases the amplitude and frequency
 CC of spontaneous contractions and tonus of hindgut muscle.

CC -!- SUBCELLULAR LOCATION: Brain.

CC -!- TISSUE SPECIFICITY: Brain.

CC -!- MASS SPECTROMETRY: MW=1076.9; METHOD=MALDI.

CC -!- SIMILARITY: SOME SIMILARITY TO TACHYKININS.

KW Tachykinin; Neuropeptide; Amidation.

FT MOD_RES 10 10

SQ SEQUENCE 10 AA; 1076 MW; 95410371E9C87685 CRC64;

Query Match 28.0%; Score 14; DB 1; Length 10;

Best Local Similarity 50.0%; Pred. No. 4.9e+03;

Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 7 GPXV 10

DB 1 GPSM 4

RESULT 7

ID COXO RAT STANDARD; PRT; 10 AA.

AC P80432;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Cytochrome c oxidase polypeptide VIIC, mitochondrial (EC 1.9.3.1)

DE (VIIC) (Fragment).

GN COX7C OR COX7C1.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE.

RC STRAIN=Wistar; TISSUE=Heart, and Liver;

RX MEDLINE=95324529; PubMed=7601105;

RA Schaeffer H., Noack H., Halangk W., Brandt U., von Jagow G.;

RT "Cytochrome-c oxidase in developing rat heart. Enzymic properties and

RT amino-terminal sequences suggest identity of the fetal heart and the

RT adult liver isoform.";

RL Eur. J. Biochem. 230:1235-241(1995).

CC -!- FUNCTION: This protein is one of the nuclear-coded polypeptide

CC chains of cytochrome c oxidase, the terminal oxidase in

CC mitochondrial electron transport.

CC -!- CATALYTIC ACTIVITY: 4 ferrocycytochrome c + O(2) = 4 ferricytochrome

CC c + 2 H(2)O.

CC -!- SIMILARITY: Belongs to the cytochrome c oxidase VIIC family.

DR PIR; S65388; S65388.

KW Oxidoreductase; Mitochondrion.

FT NON_TER 10 10

SQ SEQUENCE 10 AA; 1117 MW; 126DE767687B1B0B CRC64;

Query Match

Best Local Similarity 26.0%; Score 13; DB 1; Length 10;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 GP 8

DB 6 GP 7

RESULT 8

COXO THUCB

ID COXO THUCB STANDARD; PRT; 10 AA.

AC P80982;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Cytochrome c oxidase polypeptide VIIC (EC 1.9.3.1) (Fragment).

OS Thunnus obesus (Bigeye tuna).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;

OC Scombridae; Thunnus.

OX NCBI_TaxID=8241;

RN [1]

RP SEQUENCE.

RC TISSUE=Heart, and Liver;

RC MEDLINE=97454291; PubMed=9310366;

RX Arnold S., Lee I., Kim M., Song E., Linder D., Lottspeich F.;

RA Kadenbach B.;

RT "The subunit structure of cytochrome-c oxidase from tuna heart and

RL Eur. J. Biochem. 248:99-103(1997).

CC -!- FUNCTION: This protein is one of the nuclear-coded polypeptide

CC chains of cytochrome c oxidase, the terminal oxidase in

CC mitochondrial electron transport.

CC -!- CATALYTIC ACTIVITY: 4 ferrocycytochrome c + O(2) = 4 ferricytochrome

CC c + 2 H(2)O.

CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.

CC -!- SIMILARITY: Belongs to the cytochrome c oxidase VIIC family.

DR PIR; S77990; S77990.

KW Oxidoreductase; Inner membrane; Mitochondrion.

FT NON_TER 10 10

SQ SEQUENCE 10 AA; 1059 MW; 126DE767687B1DCB CRC64;

Query Match

Best Local Similarity 25.0%; Score 13; DB 1; Length 10;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 GP 8

DB 6 GP 7

RESULT 9

PNEU HUMAN

ID PNEU HUMAN STANDARD; PRT; 10 AA.

AC P22103;

DT 01-AUG-1991 (Rel. 19, Created)

DT 01-AUG-1991 (Rel. 19, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Pneumadin (PNN).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE.

RC TISSUE=Lung;

RC MEDLINE=9110910; PubMed=2274581;

RA Batra V.K., Mathur M., Mir S.A., Kapoor R., Kumar M.A.;

RT "Pneumadin: a new lung peptide which triggers antidiuresis.";

RL Regul. Pept. 30:77-87(1990).

CC -!- FUNCTION: Antidiuretic peptide that triggers the release of ADH.

CC PIR; B33143; B33143.

DR GO; GO:0030103; P:vasopressin secretion; NAS.

KW Amidation.

FT MOD_RES 10 10

SQ SEQUENCE 10 AA; 956 MW; 640378DAA723276B CRC64;

Query Match

Best Local Similarity 25.0%; Score 13; DB 1; Length 10;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 DSG 6
|:|
Db 7 DAG 9

RESULT 10

PNEU_RAT
ID_PNEU_RAT STANDARD; PRT; 10 AA.
AC P21956;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pneumadin (PNM).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Lung;
RX MEDLINE=91110910; PubMed=2274681;
RA Batra V.K., Mathur M., Mir S.A., Kapoor R., Kumar M.A.;
RT "Pneumadin: a new lung peptide which triggers antidiuresis.";
RL Regul. Pept. 30:77-87(1990).
CC -!- FUNCTION: This antidiuretic peptide triggers the release of ADH.
DR PIR; A33143; A33143.
KW Amidation.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1048 MW; 641D00DAA723276B CRC64;

Query Match 26.0%; Score 13; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 7.4e-03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 DSG 6
|:|
Db 7 DAG 9

RESULT 11

TKS2_AEDAE
ID_TKS2_AEDAE STANDARD; PRT; 10 AA.
AC P42635;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Sialokin II.
OS Aedes aegypti (Yellowfever mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.
OX NCBI_TaxID=7159;
RN [1]
RP SEQUENCE.
RC STRAIN=Rockefeller; TISSUE=Salivary gland;
RX MEDLINE=94105119; PubMed=8278354;
RA Champagne D.E., Ribeiro J.M.C.;
RT "Sialokin II and II: vasodilatory tachykinins from the yellow fever mosquito Aedes aegypti.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:138-142(1994).
CC -!- FUNCTION: Vasodilatory peptide. May activate macrophages at the site of feeding.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the tachykinin family.
DR PIR; B49581; B49581.
DR InterPro; IPR002040; Tachy Neurokinin.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1146 MW; 3DC77C6B59C33AAB CRC64;

Query Match 26.0%; Score 13; DB 1; Length 10;

Best Local Similarity 66.7%; Pred. No. 7.4e-03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 DSG 6
|:|
Db 1 DIG 3

RESULT 12

COXH_ONCMY
ID_COXH_ONCMY STANDARD; PRT; 10 AA.
AC P80331;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE Cytochrome c oxidase polypeptide Vic (EC 1.9.3.1) (Fragment).
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=94237150; PubMed=8181469;
RA Freund R., Kadenbach B.;
RT "Identification of tissue-specific isoforms for subunits Vb and VIIa of cytochrome c oxidase isolated from rainbow trout.";
RL Eur. J. Biochem. 221:1111-1116(1994).
CC -!- FUNCTION: This protein is one of the nuclear-coded polypeptide chains of cytochrome c oxidase, the terminal oxidase in mitochondrial electron transport.
CC -!- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) = 4 ferricytochrome c + 2 H(2)O.
CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
DR PIR; S43630; S43630.
KW Oxidoreductase; Inner membrane; Mitochondrion.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 977 MW; E11B40769DC772DA CRC64;

Query Match 24.0%; Score 12; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e-04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GG 7
|:|
Db 8 GG 9

RESULT 13

CU30_LOCFMI
ID_CU30_LOCFMI STANDARD; PRT; 10 AA.
AC P11735;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Cuticle protein 30 (LM-30) (LM-ACP 30) (Fragment).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE.
RX MEDLINE=86108304; PubMed=3943519;
RA Hoejrup P., Andersen S.O., Roepstorff P.;
RT "Isolation, characterization, and N-terminal sequence studies of cuticular proteins from the migratory locust, Locusta migratoria.";
RL Eur. J. Biochem. 154:153-159(1986).
CC -!- FUNCTION: Component of the cuticle of migratory locust which contains more than 100 different structural proteins.
CC PIR; H24802; H24802.
KW Structural protein; Cuticle.

FT NON TER 10 10
SQ SEQUENCE 10 AA; 969 MW; 4973B36B58772877 CRC64;

Query Match 24.0%; Score 12; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GG 7
Db 8 GG 9

RESULT 14

FAR7 MACRS STANDARD; PRT; 10 AA.
AC P83280;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE FMRamide-like neuropeptide FLP7 (GYDRNPLRP-amide).
OS Macrobrachium rosenbergii (Giant fresh water prawn).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;
OC Palaemonoidea; Palaemonidae; Macrobrachium.
OX NCBI_TaxID=79674;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE-Eyestalk;
RX MEDLINE=21107394; PubMed=11179812;
RA Sithigorngul P., Sarathongkum W., Longyant S., Panchan N.,
RT "Three more novel FMRamide-like neuropeptide sequences from the
RT eyestalk of the giant freshwater prawn Macrobrachium rosenbergii.";
RL Peptides 22:191-197(2001).
CC -!- MASS SPECTROMETRY: MW=1244.9; METHOD=WALDI.
CC -!- SIMILARITY: Belongs to the FARP (FMRamide related peptide)
CC family.
DR GO: GO:0007218; P:neuropeptide signaling pathway; IDA.
KW Neuropeptide; Amidation.
FT MOD RES 10 10
SQ SEQUENCE 10 AA; 1244 MW; 3CFE9C29C4540AA8 CRC64;

Query Match 24.0%; Score 12; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GD 4
Db 3 GD 4

RESULT 15

FARP MYTED STANDARD; PRT; 10 AA.
AC P42580;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE FMRamide-like neuropeptide ALAGDHFRP-amide.
OS Mytilus edulis (Blue mussel).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;
OC Mytiloidea; Mytilidae; Mytilus.
OX NCBI_TaxID=6550;
RN [1]
RP SEQUENCE
RX MEDLINE=93047883; PubMed=1358534;
RA Walker R.J.;
RT "Neuroactive peptides with an RFamide or Famide carboxyl terminal."
RL Comp. Biochem. Physiol. 102C:213-222(1992).
CC -!- SIMILARITY: Belongs to the FARP (FMRamide related peptide)
CC family.
DR PIR; A58365; A58365.
KW Neuropeptide; Amidation.

FT MOD RES 10 10
SQ SEQUENCE 10 AA; 1180 MW; C2F80CC9C1EAA87D CRC64;

Query Match 24.0%; Score 12; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GD 4
Db 4 GD 5

Search completed: February 26, 2004, 09:22:04
Job time : 10.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 26, 2004, 09:16:49 ; Search time 35 Seconds
(without alignments)
90.148 Million cell updates/sec

Title: US-09-909-348-2
Perfect score: 50
Sequence: 1 CXGDSGPXV 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 603

Minimum DB seq length: 10
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp Vertebrate:*
- 14: sp Unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archheap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	40.0	10	Q9TS42	Q9TS42 sus scrofa
2	20	40.0	10	P82938	P82938 hordeum vul
3	17	34.0	10	Q9X533	Q9X533 escherichia
4	17	34.0	10	Q9X534	Q9X534 leclercia a
5	17	34.0	10	Q9UNP2	Q9UNP2 homo sapien
6	17	34.0	10	Q9UE86	Q9UE86 homo sapien
7	17	34.0	10	Q947R7	Q947R7 solanum tub
8	16	32.0	10	Q9NEY9	Q9NEY9 homo sapien
9	16	32.0	10	P82222	P82222 bombyx mori
10	16	32.0	10	Q9TU33	Q9TU33 canis famil
11	16	32.0	10	Q9QVK7	Q9QVK7 mus sp. mep
12	15	30.0	10	Q96QA7	Q96QA7 homo sapien
13	15	30.0	10	Q9P229	Q9P229 homo sapien
14	15	30.0	10	Q9S936	Q9S936 beta vulgar
15	15	30.0	10	Q9QVF0	Q9QVF0 mus sp. pro
16	15	30.0	10	Q9QVE9	Q9QVE9 mus sp. pro

17	14	28.0	10	2	Q50032	Q50032 mycobacteri
18	14	28.0	10	6	Q8MJ78	Q8MJ78 bos mutus g
19	14	28.0	10	13	Q9PRU9	Q9PRU9 sparus aura
20	13	26.0	10	2	Q8RJF1	Q8RJF1 pseudomonas
21	13	26.0	10	2	Q9X3M2	Q9X3M2 prochloroco
22	13	26.0	10	2	Q8R7J8	Q8R7J8 helicobacte
23	13	26.0	10	4	Q8R7J8	Q8R7J8 helicobacte
24	13	26.0	10	4	Q8R7J8	Q8R7J8 helicobacte
25	13	26.0	10	8	Q8SH93	Q8SH93 brookesia p
26	13	26.0	10	8	Q8SA29	Q8SA29 pyrrhobryum
27	13	26.0	10	10	Q99213	Q99213 aegilops sq
28	13	26.0	10	10	Q7Y0R0	Q7Y0R0 brassica ju
29	13	26.0	10	11	Q63389	Q63389 rattus norv
30	13	26.0	10	12	Q83378	Q83378 influenzavi
31	13	26.0	10	12	P90373	P90373 suid herpes
32	13	26.0	10	13	Q90Y93	Q90Y93 gallus gall
33	12	24.0	10	13	Q73594	Q73594 gallus gall
34	12	24.0	10	2	Q8KH99	Q8KH99 clostridium
35	12	24.0	10	2	Q52837	Q52837 rhizobium l
36	12	24.0	10	2	Q51812	Q51812 escherichia
37	12	24.0	10	4	O00493	O00493 homo sapien
38	12	24.0	10	4	Q9UCU6	Q9UCU6 homo sapien
39	12	24.0	10	5	Q7Z5A2	Q7Z5A2 homo sapien
40	12	24.0	10	6	Q8SD29	Q8SD29 trypanosoma
41	12	24.0	10	11	Q08622	Q08622 macaca mula
42	11	22.0	10	5	P82223	P82223 rattus norv
43	11	22.0	10	5	P82224	P82224 bombyx mori
44	11	22.0	10	6	Q8KP04	Q8KP04 ateles belz
45	11	22.0	10	6	Q9TR48	Q9TR48 bos taurus

ALIGNMENTS

RESULT 1

ID	Q9TS42	PRELIMINARY;	PRT;	10 AA.
AC	Q9TS42;			
DT	01-MAY-2000 (TRENBLrel. 13, Created)			
DT	01-MAY-2000 (TRENBLrel. 13, Last sequence update)			
DT	01-JUN-2002 (TRENBLrel. 21, Last annotation update)			
DE	OESTRADIOL-RECEPTOR-P2 peptide (Fragment).			
OS	Sus scrofa (Pig).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OX	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.			
NCBI	TaxID=9823;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE-91291128; PubMed=2064508;			
RA	Thole H.H., Jungblut P.W., Jakob F.;			
RT	"The proton-driven dissociation of oestradiol-receptor dimers as a			
RT	preparative tool. Isolation of a 32 kDa fragment from porcine uteri			
RL	and assignment of C-terminal origin by partial sequencing.";			
FT	Biochem. J. 276:709-714(1991).			
FT	NON_TER 1			
FT	NON_TER 10			
SQ	SEQUENCE 10 AA; 992 MW; D95E047B1451B76D CRC64;			

Query Match 40.0%; Score 20; DB 6; Length 10;
Best Local Similarity 60.0%; Pred. No. 3.3e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 DSGGP 8
DB 6 NEGGP 10

RESULT 2

ID	P82938	PRELIMINARY;	PRT;	10 AA.
AC	P82938;			
DT	01-MAR-2001 (TRENBLrel. 16, Created)			
DT	01-MAR-2001 (TRENBLrel. 16, Last sequence update)			

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DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE Unknown endosperm protein C (Fragment).
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE.
RC STRAIN=cv. BOMI; TISSUE=Starchy endosperm;
RX MEDLINE=2108911; PubMed=11271488;
RA Kristoffersen H.E., Flengsrud R.;
RT "Separation and characterization of basic barley seed proteins.";
RL Electrophoresis 21:3693-3700(2000).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
FT NON TER 10 10
SQ SEQUENCE 10 AA; 1053 MW; 95562DC40AA87AAE CRC64;

Query Match 40.0%; Score 20; DB 10; Length 10;
Best Local Similarity 75.0%; Pred. No. 3.3e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CXGD 4
DB 3 CDGD 6

RESULT 3
Q9X533 PRELIMINARY; PRT; 10 AA.
AC Q9X533;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Periplasmic mercuric ion binding protein (Fragment).
GN MERP.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=209A;
RX MEDLINE=97208220; PubMed=9055422;
RA Liebert C.A., Wireman J., Smith T., Summers A.O.;
RT "Phylogeny of mercury resistance (mer) operons of gram-negative
bacteria isolated from the fecal flora of primates.";
RL Appl. Environ. Microbiol. 63:1066-1076(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=742H;
RX MEDLINE=98027386; PubMed=9361435;
RA Wireman J., Liebert C.A., Smith T., Summers A.O.;
RT "Association of mercury resistance with antibiotic resistance in the
gram-negative fecal bacteria of primates";
RL Appl. Environ. Microbiol. 63:4494-4503(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=742H;
RX MEDLINE=20568355; PubMed=11116334;
RA Liebert C.A., Watson A.L., Summers A.O.;
RT "The quality of merC, a module of the mer mosaic.";
RL J. Mol. Evol. 51:607-622(2000).
DR EMBL; AF120965; AAD23785.1; -.
FT NON TER 1 1
SQ SEQUENCE 10 AA; 1093 MW; 3F526335A5A77B58 CRC64;

Query Match 34.0%; Score 17; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 DSGGP 8
DB 1 DAGYP 5

RESULT 5
Q9UNF2 PRELIMINARY; PRT; 10 AA.
AC Q9UNF2;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Alpha 1 collagen (Fragment).
GN COL1A1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Ratcliffe T.A., Vitz J.R., Ray D.B.;
RT "SNP located within intron 32 of human pro-alpha 1 (I) collagen gene
at 10,828 bp: cytosine replaces adenine.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.

```

```

Db 1 DAGYP 5

RESULT 4
Q9X534 PRELIMINARY; PRT; 10 AA.
AC Q9X534;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Periplasmic mercuric ion binding protein (Fragment).
GN MERP.
OS Leclercia adecarboxylata.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Leclercia.
OX NCBI_TaxID=83655;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=742H;
RX MEDLINE=97208220; PubMed=9055422;
RA Liebert C.A., Wireman J., Smith T., Summers A.O.;
RT "Phylogeny of mercury resistance (mer) operons of gram-negative
bacteria isolated from the fecal flora of primates.";
RL Appl. Environ. Microbiol. 63:1066-1076(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=742H;
RX MEDLINE=98027386; PubMed=9361435;
RA Wireman J., Liebert C.A., Smith T., Summers A.O.;
RT "Association of mercury resistance with antibiotic resistance in the
gram-negative fecal bacteria of primates";
RL Appl. Environ. Microbiol. 63:4494-4503(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=742H;
RX MEDLINE=20568355; PubMed=11116334;
RA Liebert C.A., Watson A.L., Summers A.O.;
RT "The quality of merC, a module of the mer mosaic.";
RL J. Mol. Evol. 51:607-622(2000).
DR EMBL; AF120965; AAD23785.1; -.
FT NON TER 1 1
SQ SEQUENCE 10 AA; 1093 MW; 3F526335A5A77B58 CRC64;

Query Match 34.0%; Score 17; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 DSGGP 8
DB 1 DAGYP 5

RESULT 5
Q9UNF2 PRELIMINARY; PRT; 10 AA.
AC Q9UNF2;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Alpha 1 collagen (Fragment).
GN COL1A1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Ratcliffe T.A., Vitz J.R., Ray D.B.;
RT "SNP located within intron 32 of human pro-alpha 1 (I) collagen gene
at 10,828 bp: cytosine replaces adenine.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.

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DR EMBL; AF128441; AAD32608.1; -
 KW Collagen.
 FT NON_TER 1 1
 SQ SEQUENCE 10 AA; 953 MW; 364F91A873276867 CRC64;
 Query Match 34.0%; Score 17; DB 4; Length 10;
 Best Local Similarity 75.0%; Pred. No. 1.2e+04;
 Matches ~ 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 3 GDSGG 6
 DB 7 GDRG 10

RESULT 6
 Q9UE86 PRELIMINARY; PRT; 10 AA.
 ID Q9UE86
 AC Q9UE86
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DE "A 9-base pair deletion in COL1A1 in a lethal variant of osteogenesis imperfecta."
 GN COL1A1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=92042176; PubMed=1939261;
 RX Hawkins J.R., Superti-Furga A., Steinmann B., Dalglish R.;
 RT "A 9-base pair deletion in COL1A1 in a lethal variant of osteogenesis imperfecta."
 RL J Biol Chem. 266:22370-22374 (1991).
 DR EMBL; S66556; AAB20361.1; -
 DG GO: 0005584; C:collagen type I; NAS.
 DR GO: 0005201; F:extracellular matrix structural constituent; NAS.
 DR GO: 0007155; P:cell adhesion; NAS.
 FT NON_TER 1 1
 SQ SEQUENCE 10 AA; 777 MW; 2D20F6D8676DD867 CRC64;
 Query Match 34.0%; Score 17; DB 4; Length 10;
 Best Local Similarity 50.0%; Pred. No. 1.2e+04;
 Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 3 GDSGG 8
 DB 1 GPPGAP 6

RESULT 7
 Q947R7 PRELIMINARY; PRT; 10 AA.
 ID Q947R7
 AC Q947R7
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DE SKT1 potassium channel (Fragment).
 OS Solanum tuberosum (Potato).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; asterids;
 OC lamiales; Solanales; Solanaceae; Solanum.
 OX NCBI_TaxID=4113;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zimmermann S., Hart J., Ehrhardt T., Plesch G., Mueller-Roerber B.;
 RT "Two K⁺ inward rectifiers, SKT1 and KST1, co-assemble in potato guard cells via their C-terminal interaction domain."
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF237851; AAL13169.1; -
 DG GO: 0005216; F:ion channel activity; IEA.

KW Ionic channel.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1031 MW; 84F6F1772864044A CRC64;
 Query Match 34.0%; Score 17; DB 10; Length 10;
 Best Local Similarity 60.0%; Pred. No. 1.2e+04;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 3 GDSGG 7
 DB 2 GDRG 6

RESULT 8
 Q8NEY9 PRELIMINARY; PRT; 10 AA.
 ID Q8NEY9
 AC Q8NEY9
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DE Type II hair-specific keratin (Fragment).
 GN KRTHB6.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bairwa N.K., Bamezai R.;
 RT "Study of polymorphism in the regulatory region of KRTHB6 in monilethrix samples."
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY037552; AAK68688.1; -
 DG GO: 0005882; C:intermediate filament; IEA.
 KW Keratin.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1034 MW; 9B53417EAB45B87E CRC64;
 Query Match 32.0%; Score 16; DB 4; Length 10;
 Best Local Similarity 42.9%; Pred. No. 1.8e+04;
 Matches 3; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 CXGDSGG 7
 DB 3 CGSYCGG 9

RESULT 9
 P82222 PRELIMINARY; PRT; 10 AA.
 ID P82222
 AC P82222
 DT 01-OCT-2001 (TREMBlrel. 18, Created)
 DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
 DE Unknown protein from 2D-page (Fragment).
 OS Bombyx mori (Silk moth).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Bombycoidea;
 OC Bombycidae; Bombyx.
 OX NCBI_TaxID=7091;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=XINHANG X KEMING; TISSUE=Body wall, and Fat body;
 RX MEDLINE=21177481; PubMed=11280994;
 RA Zhong B.X.;
 RT "Protein database for several tissues derived from five instar of silkworm."
 RL I Chuan Heuh Pao 28:217-224 (2001).
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1131 MW; 62CD783729D1B2CB CRC64;
 Query Match 32.0%; Score 16; DB 5; Length 10;
 Best Local Similarity 75.0%; Pred. No. 1.8e+04;

Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GPXV 10
Db 1 GPEV 4

RESULT 10
Q9TU33
ID Q9TU33 PRELIMINARY; PRT; 10 AA.
AC Q9TU33; 2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE BRCAL (Fragment).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20154965; PubMed=10690375;
RA Gray I.S., Yuzbasivan-Gurkan V.;
RT "A single nucleotide (T->G) polymorphism within intron 23 of the
RL canine BRCAL gene.";
RL Anim. Genet. 31:76-77(2000).
DR EMBL; AF159258; AAD56289.1; -.
FT NON TER 1
FT NON TER 10
SQ SEQUENCE 10 AA; 1164 MW; 2AB89C65BAAB01B3 CRC64;

Query Match 32.0%; Score 16; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DSG 6
Db 6 DSG 8

RESULT 11
Q9QVK7
ID Q9QVK7 PRELIMINARY; PRT; 10 AA.
AC Q9QVK7; 2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE MEPRIN=METALLOENDOPEPTIDASE (Fragment).
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP SEQUENCE
RX MEDLINE=91363409; PubMed=1988759;
RA Flannery A.V., Macadam G.C., Beynon R.J.;
RT "Immunological characterisation of different meprin species in mice.";
RL Biochim. Biophys. Acta 1079:119-122(1991).
FT NON TER 1
FT NON TER 10
SQ SEQUENCE 10 AA; 1138 MW; FC01BFB5BAA866D1 CRC64;

Query Match 32.0%; Score 16; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GDS 5
Db 5 GDS 7

RESULT 12

Q96QA7
ID Q96QA7 PRELIMINARY; PRT; 10 AA.
AC Q96QA7; 2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE BA151A2.1 (Cdc42 guanine exchange factor (GEF) 9 (Collybistin, PEM-2,
HPEM-2, KIAA0424)) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX Whitehead S.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL451106; CAC68408.1; -.
FT NON TER 10
SQ SEQUENCE 10 AA; 1122 MW; 39925CB878640043 CRC64;

Query Match 30.0%; Score 15; DB 4; Length 10;
Best Local Similarity 75.0%; Pred. No. 2.8e+04;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GDSG 6
Db 6 GDSG 9

RESULT 13
Q9P2Z9
ID Q9P2Z9 PRELIMINARY; PRT; 10 AA.
AC Q9P2Z9; 2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE Epidermal growth factor receptor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91337091; PubMed=1678600;
RA Humphrey P.A., Gangarosa L.M., Wong A.J., Archer G.E.,
Lund-Johansen M., Bjerkvig R., Laerum O.D., Friedman H.S.,
Bigner D.D.;
RT "Deletion-mutant epidermal growth factor receptor in human gliomas:
effects of type II mutation on receptor function.";
RL Biochem. Biophys. Res. Commun. 178:1413-1420(1991).
DR EMBL; S51343; AAB19486.2; -.
GO GO:0016021; C:integral to membrane; NAS.
GO GO:0005006; P:epidermal growth factor receptor activity; NAS.
GO GO:0008283; P:cell proliferation; NAS.
KW Receptor.
FT NON TER 1
FT NON TER 10
SQ SEQUENCE 10 AA; 1020 MW; 439DEAEAB87B1727 CRC64;

Query Match 30.0%; Score 15; DB 4; Length 10;
Best Local Similarity 66.7%; Pred. No. 2.8e+04;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CXG 3
Db 7 CTG 9

RESULT 14
Q9S936
ID Q9S936 PRELIMINARY; PRT; 10 AA.
AC Q9S936;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE H(+) translocating (Pyrophosphate-ENERGIZED) inorganic pyrophosphatase
 DE beta-2 polypeptide (BC 3.6.1.1) (Fragment).
 OS Beta vulgaris (sugar beet).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllales; Amaranthaceae; Beta.
 OX NCBI_TaxID=161934;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92179265; PubMed=1311852;
 RA Sarafian V., Kim Y., Poole R.J., Rea P.A.;
 RT "Molecular cloning and sequence of cDNA encoding the pyrophosphate-
 RT energized vacuolar membrane proton pump of Arabidopsis thaliana.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:1775-1779(1992).
 DR PIR: B38230; B38230.
 DR GO: GO:0004427; F:inorganic diphosphatase activity; IEA.
 SQ SEQUENCE 10 AA; 1017 MW; 2BC8A4A87041AAA8 CRC64;

Query Match 30.0%; Score 15; DB 10; Length 10;
 Best Local Similarity 60.0%; Pred. No. 2.8e+04;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 GDSGG 7
 ||:
 Db 3 GDTIG 7

RESULT 15

Q9QVF0
 ID Q9QVF0 PRELIMINARY; PRT; 10 AA.
 AC Q9QVF0;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Protamine NP2 intermediate protein PMP2/5 (Fragment).
 OS Mus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10095;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92174934; PubMed=1541289;
 RA Chauviere M., Martinge A., Debarle M., Sautiere P., Chevaillier P.;
 RT "Molecular characterization of six intermediate proteins in the
 RT processing of mouse protamine P2 precursor.";
 RL Eur. J. Biochem. 204:759-765(1992).
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1125 MW; 9E14CE687B05A775 CRC64;

Query Match 30.0%; Score 15; DB 11; Length 10;
 Best Local Similarity 75.0%; Pred. No. 2.8e+04;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 SGGF 8
 ||:
 Db 5 SEGF 8

Search completed: February 26, 2004, 09:23:29
 Job time : 36 secs

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OM protein - protein search, using sw model
Run on: February 26, 2004, 09:00:54 ; Search time 48.5 Seconds
(without alignments)
58.257 Million cell updates/sec

Title: US-09-909-348-2
Perfect score: 50
Sequence: 1 CXGDSGXPV 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 94656

Minimum DB seq length: 10
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	92.0	10	5 AAU78372	Aau78372 Serine es
2	46	92.0	10	5 AAU78373	Aau78373 Serine es
3	46	92.0	10	5 AAE20156	Aae20156 Serine es
4	46	92.0	10	5 AAE20155	Aae20155 Serine es
5	46	92.0	10	7 ABB80261	Abb80261 Serine es
6	46	92.0	10	7 ABB80262	Abb80262 Serine es
7	43	86.0	10	4 AAB35464	Aab35464 Human mem
8	32	64.0	10	4 AAG94412	Aag94412 Human com
9	29	58.0	10	2 AAR61594	Aar61594 Peptide f
10	29	58.0	10	2 AAR96844	Aar96844 N-gonorrh
11	29	58.0	10	4 AAJ01260	Aaj01260 Hepatitis
12	29	58.0	10	4 AAJ00701	Aaj00701 Hepatitis
13	29	58.0	10	4 AAJ01934	Aaj01934 Hepatitis
14	29	58.0	10	4 AAJ01082	Aaj01082 Hepatitis
15	28	56.0	10	2 AAR11746	Aar11746 Cyclic pl
16	28	56.0	10	2 AAR11747	Aar11747 Cyclic pl
17	28	56.0	10	2 AAW79650	Aaw79650 N-alpha-A
18	28	56.0	10	2 AAW79652	Aaw79652 N-alpha-A
19	28	56.0	10	2 AAW79651	Aaw79651 N-alpha-A
20	28	56.0	10	4 AAG97390	Aag97390 Human com
21	28	56.0	10	7 ADD69406	Add69406 Angiopoie
22	27	54.0	10	4 AAG97589	Aag97589 Human com
23	27	54.0	10	4 AAG97590	Aag97590 Human com
24	27	54.0	10	5 AAE28776	Aae28776 Human CAS
25	26	52.0	10	2 AAR76887	Aar76887 Glutathio

26	26	52.0	10	2 AAU05434	Aau05434 GST-bindi
27	25	50.0	10	2 AAU52272	Aau52272 MAGE-6 de
28	25	50.0	10	2 AAU47394	Aay47394 Immunogen
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44	24	48.0	10	2 AAR10181	Aar10181 RGD-contg
45	24	48.0	10	2 AAU03419	Aau03419 Fibrinect

ALIGNMENTS

RESULT 1
AAU78372
ID AAU78372 standard; peptide; 10 AA.
XX
AC AAU78372;
XX
DT 18-JUN-2002 (first entry)
XX
DE Serine esterase conserved sequence #1.
XX

Serine esterase; osteopathic; thrombin; receptor; agonist;
KW bone growth stimulation; osteoinduction; farm animal; companion animal;
KW laboratory animal; bone graft; segmental bone gap; bone void;
KW non-union fracture.
XX
OS Synthetic.
XX
PN WO200205836-A2.
XX
PD 24-JAN-2002.
XX

PF 18-JUL-2001; 2001WO-US022641.

PR 19-JUL-2000; 2000US-0219300P.

PA (TEXA) UNIV TEXAS SYSTEM.

PI Carney DH, Crowther RS, Simmons DJ, Yang J, Redin WR;

XX WPI; 2002-303796/34.

DR Stimulating bone growth at a site in a subject in need of osteoinduction,
PT such as a site of bone graft, segmental bone gap, bone void or non-union
PT structure, by administering agonist of activated thrombin receptor.
XX
XX Claim 6; Page 21; 27pp; English.

PS The invention describes a method of stimulating bone growth at a site in

CC a subject in need of osteoinduction. The method involves administering an
CC agonist to stimulate bone growth at a site in a subject (e.g. a farm
CC animal, companion animal or laboratory animal), in need of
CC osteoinduction, such as the site in need of a bone graft in a subject, a
CC segmental bone gap, a bone void or a non-union fracture. This sequence
CC represents a serine esterase conserved sequence obtained from a serine
CC esterase that can stimulate or activate the non-proteolytically activated
XX thrombin receptor
XX Sequence 10 AA;

SQ

Query Match 92.0%; Score 46; DB 5; Length 10;
 Best Local Similarity 80.0%; Pred. No. 18;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CXGDSGGPXV 10
 DB 1 CEGDSGGPFV 10

RESULT 2

AAU78373
 ID AAU78373 standard; peptide; 10 AA.

XX AC AAU78373;
 XX DT 18-JUN-2002 (first entry)

DE DE Serine esterase conserved sequence #2.

XX KW Serine esterase; osteopathic; thrombin; receptor; agonist;
 KW bone growth stimulation; osteoinduction; farm animal; companion animal;
 KW laboratory animal; bone graft; segmental bone gap; bone void;
 KW non-union fracture.

XX OS Synthetic.

XX FH Key Location/Qualifiers
 FT Misc-difference 2
 FT FT /label= Glu, Gln
 FT FT Misc-difference 9
 FT FT /label= Phe, Met, Leu, His, Val

XX FN WO200205836-A2.
 XX PD 24-JAN-2002.

XX PF 18-JUL-2001; 2001WO-US022641.
 XX PR 19-JUL-2000; 2000US-0219300P.

XX PA (TEXA) UNIV TEXAS SYSTEM.
 XX PI Carney DH, Crowther RS, Simmons DJ, Yang J, Redin WR;
 XX DR WPI; 2002-303796/34.

XX ST Stimulating bone growth at a site in a subject in need of osteoinduction,
 PT such as a site of bone graft, segmental bone gap, bone void or non-union
 PT structure, by administering agonist of activated thrombin receptor.

XX PS Claim 8; Page 22; 27pp; English.

XX CC The invention describes a method of stimulating bone growth at a site in
 CC a subject in need of osteoinduction. The method involves administering an
 CC agonist to stimulate bone growth at a site in a subject (e.g. a farm
 CC animal, companion animal or laboratory animal), in need of
 CC osteoinduction, such as the site in need of a bone graft in a subject, a
 CC segmental bone gap, a bone void or a non-union fracture. This sequence
 CC represents a serine esterase conserved sequence obtained from a serine
 CC esterase that can stimulate or activate the non-protocytically activated
 CC thrombin receptor

XX SQ Sequence 10 AA;

Query Match 92.0%; Score 46; DB 5; Length 10;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXGDSGGPXV 10
 DB 1 CEGDSGGPXV 10

RESULT 3

AAE20156
 ID AAE20156 standard; peptide; 10 AA.

XX AC AAE20156;
 XX DT 18-JUN-2002 (first entry)

DE DE Serine esterase conserved peptide #2.

XX KW Cartilage growth; cartilage repair; arthritic joint; traumatic injury;
 KW non-protocytically activated thrombin receptor; NPAR; chondrocyte;
 KW therapy; implantation; serine esterase conserved peptide.

XX OS Unidentified.

XX FH Key Location/Qualifiers
 FT Misc-difference 2
 FT FT /label= Glu, Gln
 FT FT Misc-difference 9
 FT FT /label= Phe, Met, Leu, His, Val

XX FN WO200207748-A2.
 XX PD 31-JAN-2002.

XX PF 19-JUL-2001; 2001WO-US022668.
 XX PR 20-JUL-2000; 2000US-0219800P.

XX PA (TEXA) UNIV TEXAS SYSTEM.
 XX PI Carney DH, Crowther RS, Stiernberg J, Bergmann J;
 XX DR WPI; 2002-368953/31.

XX ST Stimulating growth and repair of cartilage, useful for treating e.g.
 PT arthritis, by local administration of an agonist of non-protocytically
 PT activated thrombin receptor.

XX PS Claim 9; Page 25; 28pp; English.

XX CC The invention relates to a method of stimulating growth and repair of
 CC cartilage. The method involves administering to the site, an agonist of
 CC non-protocytically activated thrombin receptor (NPAR). The method is
 CC used in human or veterinary medicine for the treatment of arthritic
 CC joints and damage/loss of cartilage caused by traumatic injury. Also
 CC chondrocytes may be cultured in presence of NPAR agonist to provide cells
 CC for implantation at sites requiring growth/repair of cartilage. The
 CC present sequence is serine esterase conserved peptide. This sequence is
 CC present in the thrombin peptide derivatives which serve as a NPAR agonist

XX SQ Sequence 10 AA;

Query Match 92.0%; Score 46; DB 5; Length 10;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXGDSGGPXV 10
 DB 1 CEGDSGGPXV 10

RESULT 4

AAE20155
 ID AAE20155 standard; peptide; 10 AA.

XX AC AAE20155;
 XX DT 18-JUN-2002 (first entry)

DE DE Serine esterase conserved peptide #1.

XX Carilage growth; cartilage repair; arthritic joint; traumatic injury;
KW non-protolytically activated thrombin receptor; NPAR; chondrocyte;
KW therapy; implantation; serine esterase conserved peptide.
XX Unidentified.
XX WO200207748-A2.
XX 31-JAN-2002.
XX 19-JUL-2001; 2001WO-US022668.
XX 20-JUL-2000; 2000US-0219800P.
XX (TEXA) UNIV TEXAS SYSTEM.
XX Carney DH, Crowther RS, Stiernberg J, Bergmann J;
XX WPI; 2002-268953/31.
XX Stimulating growth and repair of cartilage, useful for treating e.g.
PT arthritis, by local administration of an agonist of non-proteolytically
PT activated thrombin receptor.
XX Claim 7; Page 24; 28pp; English.
XX The invention relates to a method of stimulating growth and repair of
CC cartilage. The method involves administering to the site, an agonist of
CC non-protolytically activated thrombin receptor (NPAR). The method is
CC used in human or veterinary medicine for the treatment of arthritic
CC joints and damage/loss of cartilage caused by traumatic injury. Also
CC chondrocytes may be cultured in presence of NPAR agonist to provide cells
CC for implantation at sites requiring growth/repair of cartilage. The
CC present sequence is serine esterase conserved peptide. This sequence is
CC present in the thrombin peptide derivatives which serve as a NPAR agonist
XX SQ Sequence 10 AA;
XX
Query Match 92.0%; Score 46; DB 5; Length 10;
Best Local Similarity 80.0%; Pred. No. 18;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CXGDSGGPFXV 10
Db 1 CEGDSGGPFV 10
RESULT 5
ABB80261
ID ABB80261 standard; peptide; 10 AA.
XX AC ABB80261;
XX DT 18-DEC-2003 (first entry)
XX Serine esterase conserved sequence #1.
XX Serine esterase; conserved domain; thrombin peptide; stimulation; bone;
KW cartilage; growth; repair; bone graft; segmental gap; bone void;
KW non-union fracture; arthritic joint; arthritis; damage; traumatic injury;
KW culture; chondrocyte; joint bio mechanics; osteoarthritis.
XX Mammal sp.
XX WO2003061690-A1.
XX 31-JUL-2003.
XX 17-JAN-2002; 2002WO-US001451.
XX 17-JAN-2002; 2002WO-US001451.
XX 17-JAN-2002; 2002WO-US001451.

PA (TEXA) UNIV TEXAS SYSTEM.
XX Carney DH, Crowther RS, Simmons DJ, Yang J, Redin WR;
PI Stiernberg J, Bergmann J;
XX WPI; 2003-721552/68.
XX Stimulation of bone growth and cartilage formation in e.g. bone graft and
PT arthritic joints involves administration of a thrombin derivative
PT peptide.
XX Disclosure; Page 8; Opp; English.
XX The sequences given in ABB80261-62 represent serine esterase conserved
CC domains. These peptide are used as part of the thrombin peptides
CC derivatives of the invention for stimulating bone growth. The thrombin
CC peptides of the invention have the formula: App-Ala-R, where R is a
CC serine esterase conserved domain. These peptides are used for stimulating
CC bone growth and cartilage growth or repair in e.g. bone graft, segmental
CC gap in a bone, bone void, at a non-union fracture, arthritic joints, and
CC sites treated for cartilage damage or loss due to traumatic injury, and
CC for culturing chondrocytes in vitro. The thrombin derivative peptide
CC improves the quality of repair tissue, leads to more durable and
CC functional restoration of joint bio mechanics, reduces the incidence of
CC osteoarthritis in patients suffering from traumatic cartilage injuries
CC and accelerates the rate of normal fracture healing in fracture or small
CC gap defects
XX SQ Sequence 10 AA;
XX
Query Match 92.0%; Score 46; DB 7; Length 10;
Best Local Similarity 80.0%; Pred. No. 18;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CXGDSGGPFXV 10
Db 1 CEGDSGGPFV 10
RESULT 6
ABB80262
ID ABB80262 standard; peptide; 10 AA.
XX AC ABB80262;
XX DT 18-DEC-2003 (first entry)
XX Serine esterase conserved sequence #2.
XX Serine esterase; conserved domain; thrombin peptide; stimulation; bone;
KW cartilage; growth; repair; bone graft; segmental gap; bone void;
KW non-union fracture; arthritic joint; arthritis; damage; traumatic injury;
KW culture; chondrocyte; joint bio mechanics; osteoarthritis.
XX Mammal sp.
XX Key Location/Qualifiers
XX Misc-difference 2 /label= Glu, Gln
XX Misc-difference 9 /label= Phe, Met, Leu, His, Val
XX WO2003061690-A1.
XX 31-JUL-2003.
XX 17-JAN-2002; 2002WO-US001451.
XX 17-JAN-2002; 2002WO-US001451.
XX (TEXA) UNIV TEXAS SYSTEM.
XX Carney DH, Crowther RS, Simmons DJ, Yang J, Redin WR;

DE Hepatitis C virus epitope #1073.
 XX
 KW Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
 XX antiviral.
 XX
 XX Hepatitis C virus.
 XX OS
 PN WO200121189-A1.
 XX
 XX
 PD 29-MAR-2001.
 XX
 XX
 PF 19-JUL-2000; 2000WO-US019774.
 XX
 XX
 PR 19-JUL-1999; 99US-00357737.
 XX
 XX (EPIM-) EPIMUNE INC.
 XX
 PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 PI Baker DW, Celis E, Kubo RT, Grey HW;
 XX
 DR WPI; 2001-308046/32.
 XX
 XX
 PT A new composition useful as a vaccines against hepatitis C virus.
 XX
 PS Disclosure; Page 127; 214pp; English.
 XX
 CC The present invention describes a composition comprising a prepared
 CC hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
 CC These are derived from HCV HLA-binding motifs. They are useful in
 CC vaccines for the prevention and treatment of HCV infection in humans. The
 CC present sequence is an epitope used in the disclosure of the invention
 XX
 XX Sequence 10 AA;
 SQ
 Query Match 58.0%; Score 29; DB 4; Length 10;
 Best Local Similarity 83.3%; Pred. No. 2.2e+03;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 3 GDSGGP 8
 DB 4 GSSGGP 9
 RESULT 15
 AAR11746
 ID AAR11746 standard; peptide; 10 AA.
 XX
 AC AAR11746;
 XX
 DT 25-MAR-2003 (revised)
 DT 05-JUL-1991 (first entry)
 XX
 XX
 DE Cyclic platelet aggregation inhibitor - example #3.
 XX
 KW Myocardial infarction; deep vein thrombosis; pulmonary embolism; stroke.
 XX
 OS Synthetic.
 XX
 XX EP425212-A.
 PN
 XX PD 02-MAY-1991.
 XX
 XX
 PF 22-OCT-1990; 90EP-00311537.
 XX
 PR 23-OCT-1989; 89US-00425906.
 XX
 PA (SMIK) SMITHKLINE BEECHAM.
 PA (ALIF/) ALI F E.
 XX
 PI Ali FEF, Samanen JM;
 XX
 DR WPI; 1991-126685/18.
 XX

PT New cyclic peptide(s) with Gly-asp sequence - useful as platelet
 PT aggregation inhibitors to treat myocardial infarction, deep vein
 XX thrombosis, pulmonary embolism, stroke etc.

PS Claim 9; Page 44; 55pp; English.

XX The sequence is the peptide part of the cpd.: N[alpha]-Ac-cyclo(S,S)-Cys-
 CC Arg-Gly-asp-Ser-Arg-Gly-asp-Ser-Cys-NH2 See also AAR11743-R11748 for
 CC examples. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-
 CC MAR-2003 to correct FI field.)

XX SQ Sequence 10 AA;

Query Match 56.0%; Score 28; DB 2; Length 10;
 Best Local Similarity 71.4%; Pred. No. 2.9e+03;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CXGDSGG 7
 DB 1 CRGDSRG 7

Search completed: February 26, 2004, 09:21:30
 Job time : 49.5 secs

GenCore version 5.1.6
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QM protein - protein search, using sw model

Run on: February 26, 2004, 09:23:35 ; Search time 26.5 Seconds
(without alignments)
79.680 Million cell updates/sec

Title: US-09-909-348-2

Perfect score: 50

Sequence: 1 CXGDSGGPVX 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 809742 seqs, 211153259 residues

Total number of hits satisfying chosen parameters: 31379

Minimum DB seq length: 10

Maximum DB seq length: 10

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:

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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
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8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
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11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	46	92.0	10	9	US-09-909-348-2
3	46	92.0	10	9	US-09-909-122-1
4	46	92.0	10	9	US-09-909-122-2
5	46	92.0	10	13	US-10-050-692-1
6	46	92.0	10	13	US-10-050-692-2
7	46	92.0	10	13	US-10-050-688-1
8	46	92.0	10	13	US-10-050-688-2
9	32	64.0	10	10	US-09-572-404B-606
10	28	56.0	10	10	US-09-572-404B-3584
11	27	54.0	10	10	US-09-572-404B-3784
12	27	54.0	10	10	US-09-572-404B-3785
13	26	52.0	10	9	US-09-879-957-55
14	25	50.0	10	10	US-09-572-404B-174
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16	25	50.0	10	10	US-09-572-404B-2033	Sequence 2033, Ap
17	25	50.0	10	10	US-09-572-404B-2091	Sequence 2091, Ap
18	25	50.0	10	10	US-09-572-404B-2093	Sequence 2093, Ap
19	25	50.0	10	10	US-09-572-404B-2095	Sequence 2095, Ap
20	25	50.0	10	10	US-09-572-270A-196	Sequence 196, App
21	25	50.0	10	10	US-09-572-270A-204	Sequence 204, App
22	25	50.0	10	10	US-09-572-270A-206	Sequence 206, App
23	25	50.0	10	14	US-10-155-333-9	Sequence 9, Appli
24	24	48.0	10	10	US-09-572-404B-4	Sequence 4, Appli
25	24	48.0	10	10	US-09-572-270A-277	Sequence 277, App
26	24	48.0	10	10	US-09-572-270A-281	Sequence 281, App
27	24	48.0	10	10	US-09-572-270A-283	Sequence 283, App
28	24	48.0	10	10	US-09-572-270A-285	Sequence 285, App
29	24	48.0	10	10	US-09-572-270A-293	Sequence 293, App
30	24	48.0	10	10	US-09-572-270A-295	Sequence 295, App
31	24	48.0	10	10	US-09-573-822C-496	Sequence 496, App
32	24	48.0	10	13	US-10-008-355-25	Sequence 25, Appli
33	23	46.0	10	9	US-09-879-957-54	Sequence 54, Appli
34	23	46.0	10	10	US-09-572-404B-114	Sequence 114, App
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36	23	46.0	10	10	US-09-572-404B-342	Sequence 342, App
37	23	46.0	10	10	US-09-572-404B-344	Sequence 344, App
38	23	46.0	10	10	US-09-572-404B-1306	Sequence 1306, Ap
39	23	46.0	10	10	US-09-572-404B-2218	Sequence 2218, Ap
40	23	46.0	10	10	US-09-572-404B-2332	Sequence 2332, Ap
41	23	46.0	10	10	US-09-572-404B-2668	Sequence 2668, Ap
42	23	46.0	10	10	US-09-572-404B-2798	Sequence 2798, Ap
43	23	46.0	10	10	US-09-572-404B-3352	Sequence 3352, Ap
44	23	46.0	10	10	US-09-572-404B-3354	Sequence 3354, Ap
45	23	46.0	10	10	US-09-572-404B-3356	Sequence 3356, Ap

ALIGNMENTS

RESULT 1
US-09-909-348-1
; Sequence 1, Application US/09909348
; Patent No. US20020042373A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; APPLICANT: Crowther, Roger S.
; APPLICANT: Stierberg, Janet
; APPLICANT: Bergmann, John
; TITLE OF INVENTION: Stimulation Of Cartilage Growth With Agonists
; FILE REFERENCE: 3033.1003-001
; CURRENT APPLICATION NUMBER: US/09/909,348
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/219,800
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide fragment of Thrombin
US-09-909-348-1

Query Match 92.0%; Score 46; DB 9; Length 10;
Best Local Similarity 80.0%; Pred.No. 0.28;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CXGDSGGPVX 10
DB 1 CEGDSGGPVF 10

RESULT 2
US-09-909-348-2
; Sequence 2, Application US/09909348

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Patent No. US20020042373A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; APPLICANT: Crowther, Roger S.
; APPLICANT: Stierberg, Janet
; APPLICANT: Bergmann, John
; TITLE OF INVENTION: Stimulation Of Cartilage Growth With Agonists
; FILE REFERENCE: 3033.1003-001
; CURRENT APPLICATION NUMBER: US/09/909,348
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/219,800
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 10
; TYPE: PRT
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; NAME/KEY: VARIANT
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Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 CXGDSGGGPXV 10
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US-09-909-122-1
; Sequence 1, Application US/09909122
; Patent No. US20020128202A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; APPLICANT: Crowther, Roger S.
; APPLICANT: Simmons, David J.
; APPLICANT: Yang, Jiping
; APPLICANT: Redin, William R.
; TITLE OF INVENTION: Stimulation Of Bone Growth With Thrombin
; FILE REFERENCE: 3033.1002-001
; CURRENT APPLICATION NUMBER: US/09/909,122
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/219,300
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide fragment of Thrombin
US-09-909-122-1
Query Match 92.0%; Score 46; DB 9; Length 10;
Best Local Similarity 80.0%; Pred. No. 0.28;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CXGDSGGGPXV 10
Db 1 CEGDSGGGPV 10
RESULT 4
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US-09-909-122-2
; Sequence 2, Application US/09909122
; Patent No. US20020128202A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; APPLICANT: Crowther, Roger S.
; APPLICANT: Simmons, David J.
; APPLICANT: Yang, Jiping
; APPLICANT: Redin, William R.
; TITLE OF INVENTION: Stimulation Of Bone Growth With Thrombin
; FILE REFERENCE: 3033.1002-001
; CURRENT APPLICATION NUMBER: US/09/909,122
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/219,300
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(10)
; OTHER INFORMATION: Xaa at position two is Glu or Gln
; OTHER INFORMATION: Xaa at position nine is Phe, Met, Leu, His or Val
US-09-909-122-2
Query Match 92.0%; Score 46; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CXGDSGGGPXV 10
Db 1 CXGDSGGGPXV 10
RESULT 5
US-10-050-692-1
; Sequence 1, Application US/10050692
; Publication No. US20020182205A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; APPLICANT: Crowther, Roger S.
; APPLICANT: Simmons, David J.
; APPLICANT: Yang, Jiping
; APPLICANT: Redin, William R.
; TITLE OF INVENTION: STIMULATION OF BONE GROWTH WITH THROMBIN
; FILE REFERENCE: 3033.1002-004
; CURRENT APPLICATION NUMBER: US/10/050,692
; CURRENT FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: 09/909,122
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/219,300
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fragment of human prothrombin
US-10-050-692-1
Query Match 92.0%; Score 46; DB 13; Length 10;
Best Local Similarity 80.0%; Pred. No. 0.28;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CXGDSGGGPXV 10
```



```
Db      1  CEGDSGGPFV 10
;
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide fragment of thrombin
US-10-050-688-1

Query Match      92.0%; Score 46; DB 13; Length 10;
Best Local Similarity 80.0%; Pred. No. 0.28;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1  CXGDSGGPXV 10
        |||||
DB      1  CEGDSGGPFV 10

RESULT 8
US-10-050-688-2
; Sequence 2, Application US/10050688
; Publication No. US20020198154A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; APPLICANT: Crowther, Roger S.
; APPLICANT: Stierberg, Janet
; APPLICANT: Bergmann, John
; TITLE OF INVENTION: STIMULATION OF CARTILAGE GROWTH WITH
; TITLE OF INVENTION: AGONISTS OF THE NON-PROTEOLYTICALLY ACTIVATED THROMBIN
; FILE REFERENCE: 3033.1003-004
; CURRENT APPLICATION NUMBER: US/10/050,688
; CURRENT FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: 09/909,348
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/219,800
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide fragment of thrombin
; NAME/KEY: VARIANT
; LOCATION: (2)...(2)
; OTHER INFORMATION: Xaa = Glu or Gln
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (9)...(9)
; OTHER INFORMATION: Xaa = Phe, Met, Leu, His or Val
US-10-050-688-2

Query Match      92.0%; Score 46; DB 13; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  CXGDSGGPXV 10
        |||||
DB      1  CXGDSGGPXV 10

RESULT 9
US-09-572-404B-606
; Sequence 606, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human Patent US/09/572,404B
; CURRENT APPLICATION NUMBER: 2000-05-17
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
```

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Db      1  CEGDSGGPFV 10
;
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human fragment of prothrombin
US-10-050-692-2

Query Match      92.0%; Score 46; DB 13; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  CXGDSGGPXV 10
        |||||
DB      1  CXGDSGGPXV 10

RESULT 7
US-10-050-688-1
; Sequence 1, Application US/10050688
; Publication No. US20020198154A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; APPLICANT: Crowther, Roger S.
; APPLICANT: Stierberg, Janet
; APPLICANT: Bergmann, John
; TITLE OF INVENTION: STIMULATION OF CARTILAGE GROWTH WITH
; TITLE OF INVENTION: AGONISTS OF THE NON-PROTEOLYTICALLY ACTIVATED THROMBIN
; FILE REFERENCE: 3033.1003-004
; CURRENT APPLICATION NUMBER: US/10/050,688
; CURRENT FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: 09/909,348
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/219,800
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 10
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; SEQ ID NO 606
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in C2 at 674-683 and may interact with Sequence
; OTHER INFORMATION: this patent.
US-09-572-404B-606

Query Match 64.0%; Score 32; DB 10; Length 10;
Best Local Similarity 71.4%; Pred. No. 53;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CXGDSGG 7
| | | | |
Db 2 CKGESGG 8

RESULT 10

US-09-572-404B-3584
; Sequence 3584, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 3584
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in PXR1 OR PEX5 at 811-820 and may interact with
; OTHER INFORMATION: Sequence 3583 in this patent.
US-09-572-404B-3584

Query Match 56.0%; Score 28; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GDSGG 7
| | | | |
Db 6 GDSGG 10

RESULT 11

US-09-572-404B-3784
; Sequence 3784, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 3784
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in ERK5 OR ERK4 at 543-552 and may interact with
; OTHER INFORMATION: Sequence 3785 in this patent.
US-09-572-404B-3784

Query Match 54.0%; Score 27; DB 10; Length 10;
Best Local Similarity 83.3%; Pred. No. 3.5e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GDSGGP 8
| | | | |
Db 3 GASGGP 8

RESULT 12

US-09-572-404B-3785
; Sequence 3785, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 3785
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in ERK5 OR ERK4 at 543-552 and may interact with
; OTHER INFORMATION: Sequence 3784 in this patent.
US-09-572-404B-3785

Query Match 54.0%; Score 27; DB 10; Length 10;
Best Local Similarity 83.3%; Pred. No. 3.5e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GDSGGP 8
| | | | |
Db 3 GASGGP 8

RESULT 13

US-09-879-957-55
; Sequence 55, Application US/09879957
; Patent No. US20020034755A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; HOFFMAN, No. US20020034755A1h
; KAY, Brian K.
; FOWLKES, Dana M.
; MCCONNELL, Stephen J.
; TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
; DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
; USING SAME

NUMBER OF SEQUENCES: 227
CORRESPONDENCE ADDRESS:
ADDRESSER: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/879,957
FILING DATE: 13-Jun-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,915
FILING DATE: 03-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-174
TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Other
LOCATION: 8
OTHER INFORMATION: Undefined
SEQUENCE DESCRIPTION: SEQ ID NO: 55:
US-09-879-957-55

Query Match 52.0%; Score 26; DB 9; Length 10;
Best Local Similarity 71.4%; Pred. No. 5.1e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CXGDSGG 7
Db 1 CMGDSL 7

RESULT 14
US-09-572-404B-174
; Sequence 174, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 174
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in EPH4 OR HTK at 974-983 and may interact with
; OTHER INFORMATION: Sequence 173 in this patent.
US-09-572-404B-174

Query Match 50.0%; Score 25; DB 10; Length 10;
Best Local Similarity 66.7%; Pred. No. 7.4e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 3 GDSGGP 8
Db 5 GGTGGP 10

RESULT 15
US-09-572-404B-2027
; Sequence 2027, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 2027
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:

OTHER INFORMATION: sequence located in CNTFR at 340-349 and may interact with Sequenc
OTHER INFORMATION: in this patent.
US-09-572-404B-2027
Query Match 50.0%; Score 25; DB 10; Length 10;
Best Local Similarity 66.7%; Pred. No. 7.4e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3 GDSGGP 8
Db 2 GSGGGP 7
Search completed: February 26, 2004, 09:32:00
Job time : 27.5 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 26, 2004, 09:19:44 ; Search time 15.5 Seconds
(without alignments)
33.307 Million cell updates/sec

Title: US-09-909-348-2
Perfect score: 50
Sequence: 1 CXGDSGPPXV 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 13857

Minimum DB seq length: 10
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Issued Patents AA.*
- 1: /cgn2_6/prodata/2/iaa/5A-COMB.pep.*
 - 2: /cgn2_6/prodata/2/iaa/5B-COMB.pep.*
 - 3: /cgn2_6/prodata/2/iaa/6A-COMB.pep.*
 - 4: /cgn2_6/prodata/2/iaa/6B-COMB.pep.*
 - 5: /cgn2_6/prodata/2/iaa/PCITUS-COMB.pep.*
 - 6: /cgn2_6/prodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	26	52.0	10	4	US-08-630-915A-55
2	25	50.0	10	2	Sequence 9, Appl
3	25	50.0	10	2	Sequence 9, Appl
4	25	50.0	10	3	Sequence 827, App
5	25	50.0	10	3	Sequence 9, Appl
6	25	50.0	10	4	Sequence 9, Appl
7	25	50.0	10	4	Sequence 9, Appl
8	24	48.0	10	1	Sequence 16, Appl
9	24	48.0	10	3	Sequence 18, Appl
10	24	48.0	10	3	Sequence 16, Appl
11	24	48.0	10	4	Sequence 16, Appl
12	24	48.0	10	4	Sequence 18, Appl
13	24	48.0	10	5	Sequence 40, Appl
14	23	46.0	10	2	Sequence 36, Appl
15	23	46.0	10	2	Sequence 7, Appl
16	23	46.0	10	3	Sequence 9, Appl
17	23	46.0	10	3	Sequence 15, Appl
18	23	46.0	10	3	Sequence 17, Appl
19	23	46.0	10	4	Sequence 15, Appl
20	23	46.0	10	4	Sequence 15, Appl
21	23	46.0	10	4	Sequence 17, Appl
22	22	44.0	10	3	Sequence 897, App
23	22	44.0	10	3	Sequence 2, Appl
24	22	44.0	10	3	Sequence 9, Appl
25	22	44.0	10	4	Sequence 58, Appl
26	22	44.0	10	4	Sequence 6, Appl
27	21.5	43.0	10	3	Sequence 65, Appl

28	21.5	43.0	10	4	US-09-910-552-65	Sequence 65, Appl
29	21	42.0	10	1	US-08-212-186A-3	Sequence 3, Appl
30	21	42.0	10	1	US-08-105-222-6	Sequence 6, Appl
31	21	42.0	10	1	US-08-462-949-6	Sequence 6, Appl
32	21	42.0	10	1	US-08-425-238-2	Sequence 2, Appl
33	21	42.0	10	1	US-08-023-764B-6	Sequence 6, Appl
34	21	42.0	10	1	US-08-442-542-32	Sequence 32, Appl
35	21	42.0	10	1	US-08-447-853-6	Sequence 6, Appl
36	21	42.0	10	1	US-08-448-209-6	Sequence 8, Appl
37	21	42.0	10	1	US-08-244-855-8	Sequence 35, Appl
38	21	42.0	10	1	US-08-575-361A-35	Sequence 7, Appl
39	21	42.0	10	2	US-08-207-481-7	Sequence 6, Appl
40	21	42.0	10	2	US-08-448-292-6	Sequence 1, Appl
41	21	42.0	10	2	US-08-596-387B-1	Sequence 6, Appl
42	21	42.0	10	2	US-08-625-695A-3	Sequence 3, Appl
43	21	42.0	10	2	US-08-647-449-29	Sequence 29, Appl
44	21	42.0	10	2	US-08-286-861-5	Sequence 5, Appl
45	21	42.0	10	3	US-08-159-339A-885	Sequence 885, App

ALIGNMENTS

RESULT 1
US-08-630-915A-55
; Sequence 55, Application US/08630915A
; Patent No. 6309820
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: HOFFMAN, No. 6309820h
APPLICANT: KAY, Brian K.
APPLICANT: FOWLES, Dana M.
APPLICANT: MCCONNELL, Stephen J.
TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
TITLE OF INVENTION: USING SAME
NUMBER OF SEQUENCES: 227
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,915A
FILING DATE: 03-APR-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Mistock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-174
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Other
LOCATION: 8
OTHER INFORMATION: Undefined
US-08-630-915A-55

Query Match 52.0%; Score 26; DB 4; Length 10;
Best Local Similarity 71.4%; Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CXGDSGG 7
DB 1 CMGDSLG 7

RESULT 2
US-08-993-738A-9
; Sequence 9, Application US/08993738A
; Patent No. 5928938
; GENERAL INFORMATION:
; APPLICANT: van der Bruggen, Pierre; DePlaan Etienne;
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolated Peptides Which Complex With
; TITLE OF INVENTION: HLA-Cw*16 Molecules, and Uses Thereof
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski L.L.P.
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage

COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993.738A
FILING DATE: 19-December-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/713.354
FILING DATE: 13-September-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5928938man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5460.1 DIV - JEL/NDH
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear

US-08-993-738A-9
Query Match 50.0%; Score 25; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 3.3e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 SGGPV 10
DB 3 SGGPRI 8

RESULT 3
US-08-159-339A-827
; Sequence 827, Application US/0815939A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esben
; TITLE OF INVENTION: HLA Binding peptides and Their

; TITLE OF INVENTION: Uses
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159.339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 827:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-159-339A-827

Query Match 50.0%; Score 25; DB 3; Length 10;
Best Local Similarity 50.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 GDSGGPV 10
DB 2 GEAGAPV 9

RESULT 4
US-08-713-354C-9
; Sequence 9, Application US/08713354C
; Patent No. 6265215
; GENERAL INFORMATION:
; APPLICANT: van der Bruggen, Pierre; DePlaan Etienne;
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolated Peptides Which Complex With
; TITLE OF INVENTION: HLA-Cw*16 Molecules, and Uses Thereof
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/713,354C
FILING DATE: 13-September-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6265215man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5460
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-713-354C-9

Query Match 50.0%; Score 25; DB 3; Length 10;
Best Local Similarity 66.7%; Pred. No. 3.3e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 SGGPXV 10
Db 3 SGGPRI 8

RESULT 5
US-09-241-268-9
Sequence 9, Application US/09241268
Patent No. 6323028
GENERAL INFORMATION:
APPLICANT: van der Bruggen, Pierre; DePlae Etienne;
APPLICANT: Boon-Falleur, Thierry
TITLE OF INVENTION: Isolated Peptides Which Complex With
TITLE OF INVENTION: HLA-Cw*16 Molecules, and Uses Thereof
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski L.L.P.
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
ZIP: 10022

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage

COMPUTER: IBM
OPERATING SYSTEM: PC-DOS

SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/241,268

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/993,738

FILING DATE: 19-December-1997

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Hanson, No. 6323028man D.

REGISTRATION NUMBER: 30,946

REFERENCE/DOCKET NUMBER: LUD 5460.1 DIV - JEL/NDH

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 688-9200

TELEFAX: (212) 838-3884

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 10 amino acids

TYPE: amino acid

TOPOLOGY: linear

US-09-241-268-9

Query Match 50.0%; Score 25; DB 4; Length 10;
Best Local Similarity 66.7%; Pred. No. 3.3e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 SGGPXV 10
Db 3 SGGPRI 8

RESULT 6
US-09-495-562-9
Sequence 9, Application US/09495562
Patent No. 6429287
GENERAL INFORMATION:
APPLICANT: van der Bruggen, Pierre; DePlae Etienne;
APPLICANT: Boon-Falleur, Thierry

TITLE OF INVENTION: Isolated Peptides Which Complex With
TITLE OF INVENTION: HLA-Cw*16 Molecules, and Uses Thereof
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski L.L.P.

STREET: 805 Third Avenue

CITY: New York City

STATE: New York

ZIP: 10022

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage

COMPUTER: IBM

OPERATING SYSTEM: PC-DOS

SOFTWARE: Wordperfect

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/495,562

FILING DATE: 01-Feb-2000

CLASSIFICATION: <UNKNOWN>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/241,268

FILING DATE: <UNKNOWN>

ATTORNEY/AGENT INFORMATION:

NAME: Hanson, No. 6429287man D.

REGISTRATION NUMBER: 30,946

REFERENCE/DOCKET NUMBER: LUD 5460.1 DIV - JEL/NDH

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 688-9200

TELEFAX: (212) 838-3884

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 10 amino acids

TYPE: amino acid

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 9:

US-09-495-562-9

Query Match 50.0%; Score 25; DB 4; Length 10;
Best Local Similarity 66.7%; Pred. No. 3.3e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 SGGPXV 10
Db 3 SGGPRI 8

RESULT 7
US-08-340-428B-40
Sequence 40, Application US/08340428B
Patent No. 5648465
GENERAL INFORMATION:
APPLICANT: MARGOLIS, Richard U.
APPLICANT: RAUCH, Uwe

APPLICANT: MARGOLIS, Renee K.

TITLE OF INVENTION: CLONING, EXPRESSION AND USES FOR A

TITLE OF INVENTION: NEUROCAN AS A CHONDROITIN SULFATE PROTEOGLYCAN

NUMBER OF SEQUENCES: 49

CORRESPONDENCE ADDRESS:

ADDRESSEE: Browdy and Neimark

STREET: 419 Seventh Street, N.W.

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/340.428B
FILING DATE: 14 No. 5648465ember 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLYING APPLICATION NUMBER: 07/922,911
FILING DATE: 03 August 1992
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: Margolis=1A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-340-428B-40

Query Match 48.0%; Score 24; DB 1; Length 10;
Best Local Similarity 50.0%; Pred. No. 4.8e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 GDSGXPV 10
DB 3 GDQGTPL 10

RESULT 8
US-08-718-323A-16
; Sequence 16, Application US/08718323A
; Patent No. 6204007
; GENERAL INFORMATION:
; APPLICANT: Raymond John Owens, Martyn Kim Robinson,
; TITLE OF INVENTION: Antibodies against E-selectin
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6204007ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/718.323A
; FILING DATE: 11-No. 6204007-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Trujillo, Doreen Yanko
; REGISTRATION NUMBER: 35,719
; REFERENCE/DOCKET NUMBER: CARP-0054
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-718-323A-16

Query Match 48.0%; Score 24; DB 3; Length 10;
Best Local Similarity 66.7%; Pred. No. 4.8e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 SGGPXV 10
DB 5 TGGPSV 10

RESULT 10
US-09-010-290-6
; Sequence 6, Application US/09010290
; Patent No. 6217846
; GENERAL INFORMATION:
; APPLICANT: Scuttle
; TITLE OF INVENTION: SYNTHETIC PEPTIDES FOR USE IN
; TITLE OF INVENTION: THROMBUS DETECTION
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:

COUNTRY: U.S.A.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/340.428B
FILING DATE: 14 No. 5648465ember 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLYING APPLICATION NUMBER: 07/922,911
FILING DATE: 03 August 1992
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: Margolis=1A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-340-428B-40

Query Match 48.0%; Score 24; DB 1; Length 10;
Best Local Similarity 50.0%; Pred. No. 4.8e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 GDSGXPV 10
DB 3 GDQGTPL 10

RESULT 8
US-08-718-323A-16
; Sequence 16, Application US/08718323A
; Patent No. 6204007
; GENERAL INFORMATION:
; APPLICANT: Raymond John Owens, Martyn Kim Robinson,
; TITLE OF INVENTION: Antibodies against E-selectin
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6204007ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/718.323A
; FILING DATE: 11-No. 6204007-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Trujillo, Doreen Yanko
; REGISTRATION NUMBER: 35,719
; REFERENCE/DOCKET NUMBER: CARP-0054
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-718-323A-16

Query Match 48.0%; Score 24; DB 3; Length 10;
Best Local Similarity 66.7%; Pred. No. 4.8e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 SGGPXV 10
DB 5 TGGPSV 10

RESULT 10
US-09-010-290-6
; Sequence 6, Application US/09010290
; Patent No. 6217846
; GENERAL INFORMATION:
; APPLICANT: Scuttle
; TITLE OF INVENTION: SYNTHETIC PEPTIDES FOR USE IN
; TITLE OF INVENTION: THROMBUS DETECTION
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Banner & Witcoff, Ltd.
STREET: 28 State St., 28th Floor
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Wordperfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,290
FILING DATE: 21-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB8914020.6
FILING DATE: 19-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB90/00933
FILING DATE: 18-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/659,343
FILING DATE: 21-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/963,127
FILING DATE: 19-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/816,922
FILING DATE: 12-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Williams, Ph.D., Kathleen A.
REGISTRATION NUMBER: 34,380
REFERENCE/DOCKET NUMBER: 3998/73503
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-227-7111
TELEFAX: 617-227-4399
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
US-09-010-290-6

Query Match 48.0%; Score 24; DB 3; Length 10;
Best Local Similarity 80.0%; Pred. No. 4.8e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CXGDS 5
| | | |
Db 5 CRGDS 9

RESULT 11
US-09-587-526-16
Sequence 16, Application US/09587526
Patent No. 6407214
GENERAL INFORMATION:
APPLICANT: Raymond John Owens, Martyn Kim Robinson,
TITLE OF INVENTION: Antibodies against E-selectin
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6407214ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM: disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/587,526
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/718,323
FILING DATE: 11-NO. 6407214-1996
ATTORNEY/AGENT INFORMATION:
NAME: Trujillo, Doreen Yanko
REGISTRATION NUMBER: 35,719
REFERENCE/DOCKET NUMBER: CARP-0054
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-587-526-16

Query Match 48.0%; Score 24; DB 4; Length 10;
Best Local Similarity 66.7%; Pred. No. 4.8e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 SGGPXV 10
| | | |
Db 5 AGGPSV 10

RESULT 12
US-09-587-526-18
Sequence 18, Application US/09587526
Patent No. 6407214
GENERAL INFORMATION:
APPLICANT: Raymond John Owens, Martyn Kim Robinson,
TITLE OF INVENTION: Antibodies against E-selectin
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6407214ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM: disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/587,526
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/718,323
FILING DATE: 11-NO. 6407214-1996
ATTORNEY/AGENT INFORMATION:
NAME: Trujillo, Doreen Yanko
REGISTRATION NUMBER: 35,719
REFERENCE/DOCKET NUMBER: CARP-0054
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-587-526-18

Query Match 48.0%; Score 24; DB 4; Length 10;
Best Local Similarity 66.7%; Pred. No. 4.8e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 SGGPXV 10
:|||||
DB 5 TGGPSV 10

RESULT 13

PCT-US93-07306-40
; Sequence 40, Application PC/TUS9307306
; GENERAL INFORMATION:
; APPLICANT: MARGOLIS, Richard U.
; APPLICANT: RAUCH, Uwe
; APPLICANT: MARGOLIS, Renee K.
; TITLE OF INVENTION: CLONING, EXPRESSION AND USES FOR A
; TITLE OF INVENTION: NEUROCAN AS A CHONDROITIN SULFATE PROTEOGLYCAN
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07306
; FILING DATE: 03-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/922,911
; FILING DATE: 03-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Townsend, Guy K.
; REGISTRATION NUMBER: 34,033
; REFERENCE/DOCKET NUMBER: Margolis=1A PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; PCT-US93-07306-40

Query Match 48.0%; Score 24; DB 5; Length 10;
Best Local Similarity 50.0%; Pred. No. 4.8e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 GDSGXPV 10
:|||||
DB 3 GDQGTPTL 10

RESULT 14

US-08-361-864-36
; Sequence 36, Application US/08361864
; Patent No. 5977064
; GENERAL INFORMATION:
; APPLICANT: Dean, Richard T
; APPLICANT: Lister-James, John
; TITLE OF INVENTION: Multimeric Polyvalent Antithrombotic
; TITLE OF INVENTION: Agents
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Allegretti & Witcoff, Ltd.
; STREET: 10 South Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/361,864
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/955,466A
; FILING DATE: 19921002
; ATTORNEY/AGENT INFORMATION:
; NAME: NO. 5977064nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 92,668
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1..5
; OTHER INFORMATION: /label= Cyclic
; OTHER INFORMATION: /note= "The sidechain sulfur of the 1st cysteine
; OTHER INFORMATION: is protected by an -CH2CO- group, that also forms
; OTHER INFORMATION: an amide bond with the N-terminus; the Y is the D
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 6..8
; OTHER INFORMATION: /label= Tc-99m-binding
; OTHER INFORMATION: /note= "The sidechain sulfur atom of each cysteine
; OTHER INFORMATION: is protected by an acetamido group; the C-terminal
; OTHER INFORMATION: cysteine is an amide"
; US-08-361-864-36

Query Match 46.0%; Score 23; DB 2; Length 10;
Best Local Similarity 80.0%; Pred. No. 6.9e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GDSGG 7
:|||||
DB 3 GDCGG 7

RESULT 15

US-08-902-367-7
; Sequence 7, Application US/08902367
; Patent No. 5997845
; GENERAL INFORMATION:
; APPLICANT: Dean, Richard T.
; APPLICANT: Lister-James, John
; APPLICANT: Civitello, Edgar R.
; TITLE OF INVENTION: Radiolabeled Compounds for Thrombus
; TITLE OF INVENTION: Imaging
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boenhen Hulbert & Berghoff
; STREET: 300 South Wacker Drive Seventh Floor
; CITY: Chicago
; STATE: Illinois

COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM: disk
MEDIUM TYPE: Floppy
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/902,367
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/462,668
FILING DATE: 05-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: No. 5997845nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 90,1104-W
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312 913 0001
TELEFAX: 312 913 0002
TELEX:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1..3
OTHER INFORMATION: /label= D-Tyr
OTHER INFORMATION: /note= "The tyrosine residue is in the D-stereo-
OTHER INFORMATION: chemical configuration"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1..5
OTHER INFORMATION: /label= Cyclic
OTHER INFORMATION: /note= "The sidechain sulfur of the Cys
OTHER INFORMATION: residue is covalently linked to the amino
OTHER INFORMATION: terminus by a -CH2CO- group."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 8..10
OTHER INFORMATION: /label= Tc-99m-chelator
OTHER INFORMATION: /note= "The sidechain sulfur atoms of both Cys
OTHER INFORMATION: residues are each protected with an
OTHER INFORMATION: acetamidomethyl group"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 10
OTHER INFORMATION: /label= Amide
OTHER INFORMATION: /note= "The carboxyl terminus is modified to an
OTHER INFORMATION: amide"
US-08-902-367-7
Query Match 46.0%; Score 23; DB 2; Length 10;
Best Local Similarity 80.0%; Pred. No. 6.9e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 3 GDSGG 7
Db 3 GDCGG 7
Search completed: February 26, 2004, 09:24:50
Job time : 16.5 secs

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OM protein - protein search, using sw model

Run on: February 26, 2004, 09:31:00 ; Search time 21 Seconds
(without alignments)
18,322 Million cell updates/sec

Title: US-09-909-348-3

Perfect score: 21

Sequence: 1 RGDA 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 63

Minimum DB seq length: 4
Maximum DB seq length: 4

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR1.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	12	57.1	4	2	PT0711		T-cell receptor be
2	11	52.4	4	2	S47552		ubiquitin - rat
3	8	38.1	4	2	D41654		hypothetical prote
4	8	38.1	4	2	PT0677		T-cell receptor be
5	7	33.3	4	1	EXAA		antho-RFamide neur
6	7	33.3	4	2	A25844		antho-RFamide neu
7	7	33.3	4	2	A32480		achatin-I - giant
8	7	33.3	4	2	S09478		globulin IV alpha
9	6	28.6	4	2	A32039		tyrosine-melanocyt
10	6	28.6	4	2	PT0140		carbon-monoxide de
11	6	28.6	4	2	I40697		biotin A - Citroba
12	6	28.6	4	2	A41890		protein D - Escher
13	6	28.6	4	2	T30569		hypothetical prote
14	6	28.6	4	2	I38888		COI intron 16 prot
15	6	28.6	4	2	A34626		RPC4-related neuro
16	6	28.6	4	2	I51049		metallothionein-A
17	6	28.6	4	2	S39390		myosin-light-chain
18	6	28.6	4	2	PT0240		Ig heavy chain CRD
19	6	28.6	4	2	PT0271		Ig mu chain V regi
20	6	28.6	4	2	S43959		Ig mu chain V regi
21	6	28.6	4	2	A53284		T-cell receptor be
22	6	28.6	4	2	B53284		T-cell receptor be
23	6	28.6	4	2	PT0696		T-cell receptor be
24	6	28.6	4	2	PT0633		T-cell receptor be
25	6	28.6	4	2	PT0698		T-cell receptor be
26	6	28.6	4	2	PT0706		T-cell receptor be
27	6	28.6	4	2	PT0675		T-cell receptor be
28	6	28.6	4	2	PT0721		T-cell receptor be
29	6	28.6	4	2	PT0566		T-cell receptor be

protein-glutamine
phagocytosis-stimu
cardioexcitatory n
hypothetical prote
phospholipase C (B
neuropeptide Antho
FMRamide - polych
protamine p1 - ora
protamine p1 - Cer
protamine p1 - sav
thyroglobulin - do
carbon-monoxide de
gamma subunit of p
glucan 1,4-alpha-g
neuropeptide Antho
T-cell receptor be

ALIGNMENTS

RESULT 1

PT0711
T-cell receptor beta chain V-D-J region (120-2J) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0607; PT0674; PT0678; PT0570; PT0711; PT0710
J. Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; UID:91277601; PMID:1711558
A;Accession: PT0607
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-4 <FE1>
A;Experimental source: newborn thymus, strain BALB/c, 120-2J
A;Accession: PT0674
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-4 <FE2>
A;Experimental source: day 18 fetal thymus, strain BALB/c, 140-1G
A;Accession: PT0678
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-4 <FE3>
A;Experimental source: day 18 fetal thymus, strain BALB/c, 154-1L
A;Accession: PT0570
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-4 <FE4>
A;Experimental source: day 19 fetal thymus, strain BALB/c, 141-1I
A;Accession: PT0711
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-4 <FE5>
A;Experimental source: newborn thymus, strain BALB/c (clones 161-2AE and 161-2AF)
C;Keywords: T-cell receptor

Query Match 57.1%; Score 12; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GD 3

Db 3 GD 4

RESULT 2

S47552
ubiquitin - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 17-Mar-1999
C;Accession: S47552

R;Hubbard, M.J.; Carne, A.
 Biochim. Biophys. Acta 1200, 191-196, 1994
 A;Title: Differential feeding-related regulation of ubiquitin and calbindin(9kDa) in rat
 A;Reference number: S47552; PMID:94304928; PMID:8031840
 A;Accession: S47552
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-4 <HB>

Query Match 52.4%; Score 11; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RG 2
 ||
 2 RG 3

Db

RESULT 3
 D41654
 Hypothetical protein (sodC 5' region) - Haemophilus parainfluenzae (fragment)
 C;Species: Haemophilus parainfluenzae.
 C;Date: 12-Jun-1992 #sequence_revision 12-Jun-1992 #text_change 24-Feb-1995
 A;Accession: D41654
 R;Kroll, J.S.; Langford, P.R.; Loynds, B.M.
 J. Bacteriol. 173, 7449-7457, 1991
 A;Title: Copper-zinc superoxide dismutase of Haemophilus influenzae and Haemophilus para
 A;Reference number: A41654; PMID:92041655; PMID:1938942
 A;Accession: D41654
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-4 <KRO>

Query Match 38.1%; Score 8; DB 2; Length 4;
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RGD 3
 ||
 2 RFD 4

Db

RESULT 4
 PT0677
 T-cell receptor beta chain V-D-J region (126-1BG) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 A;Accession: PT0558; PT0677
 R;Feeney, A.J.
 J. Exp. Med. 174, 115-124, 1991
 A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
 A;Reference number: PT0509; PMID:91277601; PMID:1711558
 A;Accession: PT0558
 A;Status: translation not shown
 A;Molecule type: mRNA
 A;Residues: 1-4 <FE>
 A;Experimental source: day 18 fetal thymus, strain BALB/c, 126-1BG
 A;Accession: PT0677
 A;Status: translation not shown
 A;Molecule type: DNA
 A;Residues: 1-4 <FE>
 A;Experimental source: day 18 fetal thymus, strain BALB/c, 140-1BH
 C;Keywords: T-cell receptor

Query Match 38.1%; Score 8; DB 2; Length 4;
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GD 3
 ||
 3 GE 4

Db

RESULT 5
 ECXAA
 Antho-RFamide neuropeptide - sea anemone (Anthopleura elegantissima)
 C;Species: Anthopleura elegantissima
 C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 08-Dec-1995
 A;Accession: A26666
 R;Grimmelikhuijzen, C.J.P.; Graff, D.
 Proc. Natl. Acad. Sci. U.S.A. 83, 9817-9821, 1986
 A;Title: Isolation of <Glu-Gly-Arg-Phe-NH2 (Antho-RFamide), a neuropeptide from sea anem
 A;Reference number: A26666; PMID:87092339; PMID:2879288
 A;Accession: A26666
 A;Molecule type: protein
 A;Residues: 1-4 <GRI>
 C;Comment: The function of this peptide is not known but it could act as a transmitter a
 C;Superfamily: RFamide neuropeptide
 C;Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F;4/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 33.3%; Score 7; DB 1; Length 4;
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RG 2
 ||
 1 QG 2

Db

RESULT 6
 A25844
 auto-RF amide neuropeptide - sea pansy (Renilla koellikeri)
 C;Species: Renilla koellikeri (Koelliker's sea pansy)
 C;Date: 21-May-1988 #sequence_revision 30-Sep-1993 #text_change 11-Jul-1997
 A;Accession: A25844
 R;Grimmelikhuijzen, C.J.P.; Groeger, A.
 FEBS Lett. 211, 105-108, 1987
 A;Title: Isolation of the neuropeptide pGlu-Gly-Arg-Phe-amide from the pennatulid Renill
 A;Reference number: A25844
 A;Accession: A25844
 A;Molecule type: protein
 A;Residues: 1-4 <GRI>
 C;Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F;4/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 33.3%; Score 7; DB 2; Length 4;
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RG 2
 ||
 1 QG 2

Db

RESULT 7
 A32480
 achatin-I - giant African snail
 N;Contains: achatin-II
 C;Species: Achatina fulica (giant African snail)
 C;Date: 12-Oct-1989 #sequence_revision 12-Oct-1989 #text_change 17-Mar-1999
 A;Accession: A32480
 R;Kamatani, Y.; Minakata, H.; Kenny, P.T.M.; Iwashita, T.; Watanabe, K.; Funase, K.; Sun
 Biochem. Biophys. Res. Commun. 160, 1015-1020, 1989
 A;Title: Achatin-I, an endogenous neuroexcitatory tetrapeptide from Achatina fulica feru
 A;Reference number: A32480; PMID:89273551; PMID:2597281
 A;Accession: A32480
 A;Molecule type: protein
 A;Residues: 1-4 <KAM>
 A;Note: stereochemistry of the active form confirmed by chemical synthesis
 R;Ishida, T.; In, Y.; Inoue, M.; Yasuda-Kamatani, Y.; Minakata, H.; Iwashita, T.; Nomoto
 FEBS Lett. 307, 253-256, 1992
 A;Title: Effect of the D-Phe(2) residue on molecular conformation of an endogenous neuro

(H-Gly-Phe-Ala-Asp-OH).
 A:Reference number: A44691; MUID:92354723; PMID:1644179
 A:Contents: annotation; X-ray crystallography, 0.85 angstroms
 A:Note: achatin-II has L-phenylalanine
 C:Keywords: D-amino acid
 F:2/Modified site: D-phenylalanine (Phe) #status experimental

Query Match 33.3%; Score 7; DB 2; Length 4;
 Best Local Similarity 66.7%; Pred. No. 2.8e+05; Indels 0; Gaps 0;
 Matches 2; Conservative 0; Mismatches 1;

QY 2 GDA 4
 |
 |
 Db 1 GFA 3

RESULT 8

S09478
 globulin IV alpha subunit gamma chain, seed - cucurbit (fragment)
 N:Alternate names: IIS globulin alpha subunit gamma chain
 C:Species: Cucurbita sp. (cucurbit)
 C:Date: 21-Nov-1993 #sequence_revision 08-Nov-1996 #text_change 08-Nov-1996
 C:Accession: S09478
 R:Ohmura, M.; Hara, I.; Matsubara, H.
 Plant Cell Physiol. 21, 157-167, 1980
 A:Title: Pumpkin (Cucurbita sp.) seed globulin IV. Terminal sequences of the acidic and
 A:Reference number: S09066
 A:Accession: S09478
 A:Molecule type: protein
 A:Residues: 1-4 <OH>

Query Match 33.3%; Score 7; DB 2; Length 4;
 Best Local Similarity 50.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;
 Matches 1; Conservative 1; Mismatches 0;

QY 1 RG 2
 |
 |
 Db 2 QG 3

RESULT 9

A32039
 tyrosine-melanocyte-stimulating hormone release-inhibiting factor 1 - bovine
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 18-Aug-2000
 C:Accession: A32039
 R:Horvath, A.; Kastin, A.J.
 J. Biol. Chem. 264, 2175-2179, 1989
 A:Title: Isolation of tyrosine-melanocyte-stimulating hormone release-inhibiting factor
 A:Reference number: A32039; MUID:89123285; PMID:2563371
 A:Accession: A32039
 A:Molecule type: protein
 A:Residues: 1-4 <HOR>
 A:Experimental source: brain
 C:Superfamily: unassigned animal peptides
 C:Keywords: amidated carboxyl end
 F:4/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 28.6%; Score 6; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;
 Matches 1; Conservative 0; Mismatches 0;

QY 2 G 2
 |
 |
 Db 4 G 4

RESULT 10

FL0140
 carbon-monoxide dehydrogenase (EC 1.2.99.2) large chain - Pseudomonas carboxydohydrogena
 C:Species: Pseudomonas carboxydohydrogena
 C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 28-Apr-1993
 C:Accession: FL0140

R:Kraut, M.; Hugendieck, I.; Herwig, S.; Meyer, O.

Arch. Microbiol. 152, 335-341, 1989
 A:Title: Homology and distribution of CO dehydrogenase structural genes in carboxydohydrog
 A:Reference number: FL0138; MUID:90055678; PMID:2818128
 A:Accession: FL0140
 A:Molecule type: protein
 A:Residues: 1-4 <KRA>
 C:Comment: Carbon-monoxide dehydrogenase consists of three polypeptide chains: large, me
 C:Keywords: oxidoreductase

Query Match 28.6%; Score 6; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;
 Matches 1; Conservative 0; Mismatches 0;

QY 2 G 2
 |
 |
 Db 2 G 2

RESULT 11

I40697
 biotin A - Citrobacter freundii (fragment)
 C:Species: Citrobacter freundii
 C:Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 12-Aug-1996
 C:Accession: I40697
 R:Shiuan, D.; Campbell, A.
 Gene 67, 203-211, 1988
 A:Title: Transcriptional regulation and gene arrangement of Escherichia coli, Citrobacter
 A:Reference number: I40697; MUID:89006280; PMID:2971595
 A:Accession: I40697
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-4 <RES>
 A:Cross-references: GB:M21922; NID:G144434

Query Match 28.6%; Score 6; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;
 Matches 1; Conservative 0; Mismatches 0;

QY 3 D 3
 |
 |
 Db 3 D 3

RESULT 12

A41890
 protein D - Escherichia coli (fragment)
 C:Species: Escherichia coli
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 30-Sep-1993
 C:Accession: A41890
 R:Slettan, A.; Gebhardt, K.; Kristiansen, E.; Birkeland, N.K.; Lindqvist, B.H.
 J. Bacteriol. 174, 4094-4100, 1992
 A:Title: Escherichia coli K-12 and B contain functional bacteriophage P2 ogr genes.
 A:Reference number: A41890; MUID:92283767; PMID:1597424
 A:Accession: A41890
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-4 <SLE>
 A:Cross-references: GB:M81463

Query Match 28.6%; Score 6; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;
 Matches 1; Conservative 0; Mismatches 0;

QY 3 D 3
 |
 |
 Db 2 D 2

RESULT 13

T30569
 hypothetical protein - Emericella nidulans
 C:Species: Emericella nidulans, Aspergillus nidulans

Search completed: February 26, 2004, 09:34:52
Job time : 22 secs

C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 11-May-2000
C;Accession: T30569
R;Morrissey, J.; MacKenzie, D.A.; Parr, A.J.; Archer, D.B.
Curr. Genet. 34, 379-385, 1998
A;Title: Isolation and characterisation of the acetyl-CoA carboxylase gene from Aspergillus
A;Reference number: Z20869; MUID:99087906; PMID:9871120
A;Accession: T30569
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-4 <MOR>
A;Cross-references: EMBL:Y15996; NID:el285512; PID:el218041; PIDN:CAA75927.1

Query Match 28.6%; Score 6; DB 2; Length 4;
Best Local Similarity 100.0%; Pred.No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 G 2
Db 2 G 2

RESULT 14
I38988
COI intron 16 protein - Podospora anserina mitochondrion
C;Species: mitochondrion Podospora anserina
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-Dec-1999
C;Accession: I38988
R;Cummings, D.J.; Michel, F.; McNally, K.L.
Curr. Genet. 16, 381-406, 1989
A;Title: DNA sequence analysis of the 24.5 kilobase pair cytochrome oxidase subunit I mi
A;Reference number: A48327; MUID:90124722; PMID:2558809
A;Accession: I38988
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-4 <CUM>
A;Cross-references: GB:X55026; GB:M30937; GB:M61734
C;Genetics:
A;Genome: mitochondrion
A;Genetic code: SGC3
C;Keywords: mitochondrion

Query Match 28.6%; Score 6; DB 2; Length 4;
Best Local Similarity 100.0%; Pred.No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 G 2
Db 3 G 3

RESULT 15
A34626
RPCH-related neuropeptide - ferruginous spindle
C;Species: Fusinus ferrugineus (ferruginous spindle)
C;Date: 06-Jul-1990 #sequence_revision 06-Jul-1990 #text_change 31-Dec-1993
C;Accession: A34626
R;Kuroki, Y.; Kanda, T.; Kubota, I.; Fujisawa, Y.; Ikeda, T.; Miura, A.; Minamitake, Y.;
Biochem. Biophys. Res. Commun. 167, 273-279, 1990
A;Title: A molluscan neuropeptide related to the crustacean hormone, RPCH.
A;Reference number: A34626; MUID:90179762; PMID:2310394
A;Accession: A34626
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-4 <KUR>
C;Keywords: neuropeptide

Query Match 28.6%; Score 6; DB 2; Length 4;
Best Local Similarity 100.0%; Pred.No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 G 2
Db 3 G 3

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OM protein - protein search, using sw model

Run on: February 26, 2004, 09:24:55 ; Search time 12 Seconds
(without alignments)

17.357 Million cell updates/sec

Title: US-09-909-348-3

Perfect score: 21

Sequence: 1 RGDA 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 15

Minimum DB seq length: 4

Maximum DB seq length: 4

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	12	57.1	4	1 OCP1_OCTMI	P58648 octopus min
2	7	33.3	4	1 ACHI_ACHFU	P59004 achatina fu
3	6	28.6	4	1 DQML_PSECH	P19916 pseudomonas
4	6	28.6	4	1 EDSI_HUMAN	P02731 homo sapien
5	6	28.6	4	1 OCP3_OCTMI	P58649 octopus min
6	5	23.8	4	1 FAR3_HIRME	P42562 hirudo medi
7	5	23.8	4	1 FAR4_HIRME	P42563 hirudo medi
8	5	23.8	4	1 FLRF_HIRME	P42561 hirudo medi
9	5	23.8	4	1 FLRN_ATEL	P58707 anthopleura
10	5	23.8	4	1 FMRF_MACNI	P01162 macrocallis
11	5	23.8	4	1 FYRI_ATEL	P58706 anthopleura
12	5	23.8	4	1 TUFT_HUMAN	P01858 homo sapien
13	4	19.0	4	1 DCMS_PSECH	P19918 pseudomonas
14	4	19.0	4	1 FRKA_ATEL	P58705 anthopleura
15	1	4.8	4	1 RM01_YEAST	P36515 saccharomyc

ALIGNMENTS

RESULT 1

OCP1_OCTMI
ID OCP1_OCTMI STANDARD; PRT; 4 AA.
AC P58648;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Cardioactive peptides Ocp-1/Ocp-2.
OS Octopus minor (Octopus)
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
OC Octopodiformes; Octopoda; Incirrata; Octopodidae; Octopus.
OX NCBI_TaxID=89766;
RN [1]

RP SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION.
RC TISSUE=Brain;
RX MEDLINE=20336815; PubMed=10876044;
RA Iwakoshi E., Hisada M., Minakata H.;
RT "Cardioactive peptides isolated from the brain of a Japanese octopus,
RT Octopus minor"; 630(2000).
RL Peptides 21:623-630(2000).
CC -!- FUNCTION: Cardioactive; has both positive chronotropic and
CC inotropic effects on the heart. Ocp-2 is a 1000 time less
CC active than Ocp-1.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- PTM: Ocp-2 has L-Phe instead of D-Phe.
CC -!- MASS SPECTROMETRY: MW=395.2; METHOD=MALDI.
KW Hormone; D-amino acid.
KW MOD_RES 2
SQ SEQUENCE 4 AA; 394 MW; 6AA879C810000000 CRC64;
Query Match 57.1%; Score 12; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 GD 3
Db 3 GD 4
RESULT 2
ACHI_ACHFU
ID ACHI_ACHFU STANDARD; PRT; 4 AA.
AC P35904;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Achatin-I.
OS Achatina fulica (Giant African snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.
OX NCBI_TaxID=6530;
RN [1]
SEQUENCE, CHARACTERIZATION, AND SYNTHESIS.
RP STRAIN=Perussac; TISSUE=Ganglion;
RX MEDLINE=89273551; PubMed=2597281;
RA Kamatani Y., Minakata H., Kenny P.T.M., Iwashita T., Watanabe K.,
RA Funase K., Sun X.P., Iongisiri A., Kim K.H., Novales-Li P.,
RA Novales E.T., Kanapi C.G., Takeuchi H., Nomoto K.;
RT "Achatin-I, an endogenous neuroexcitatory tetrapeptide from Achatina
RT fulica Ferussac containing a D-amino acid residue.";
RL Biochem. Biophys. Res. Commun. 160:1015-1020(1989).
RN [2]
CHARACTERIZATION.
RP STRAIN=Perussac; TISSUE=Heart atrium;
RX MEDLINE=91264856; PubMed=1675568;
RA Fujimoto K., Kubota I., Yasuda-Kamatani Y., Minakata H., Nomoto K.,
RA Yoshida M., Harada A., Muneoka Y., Kobayashi M.;
RT "Purification of achatin-I from the atria of the African giant snail,
RT Achatina fulica, and its possible function.";
RL Biochem. Biophys. Res. Commun. 177:847-853(1991).
RN [3]
X-RAY CRYSTALLOGRAPHY.
RP MEDLINE=93014529; PubMed=1399265;
RX Ishida T., In Y., Doi M., Inoue M., Yasuda-Kamatani Y., Minakata H.,
RA Iwashita T., Nomoto K.;
RT "Crystal structure and molecular conformation of achatin-I
RT (H-Gly-D-Phe-Ala-Asp-OH), an endogenous neuropeptide containing a
RT D-amino acid residue.";
RL Int. J. Pept. Protein Res. 39:258-264(1992).
CC -!- FUNCTION: Neuroexcitatory peptide; increases the impulse frequency
CC and produces a spike broadening of the identified heart excitatory
CC neuron (PON); also enhances the amplitude and frequency of the
CC heart beat. Has also an effect on several other muscles.
CC PIR: A32480; A32480.
KW Hormone; D-amino acid.
KW MOD_RES 2
RN [1] D-PHENYLALANINE.

```
SQ SEQUENCE 4 AA; 408 MW; 6AADD9C810000000 CRC64;
Query Match 33.3%; Score 7; DB 1; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GDA 4
DB 1 GFA 3

RESULT 3
DCML_PSECH STANDARD; PRT; 4 AA.
ID DCML_PSECH STANDARD; PRT; 4 AA.
AC P19916;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Carbon monoxide dehydrogenase large chain [EC 1.2.99.2] (CO dehydrogenase subunit L) (CO-DH L) (Fragment).
GN CURL.
OS Pseudomonas carboxydohydrogena.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae.
OX NCBI_TaxID=290;
RN [1]_SEQUENCE.
RP MEDLINE=90055678; PubMed=2818128;
RA Kraut M., Hugendieck I., Herwig S., Meyer O.;
RT "Homology and distribution of CO dehydrogenase structural genes in carboxydotrophic bacteria.";
RL Arch. Microbiol. 152:335-341(1989).
CC -!- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon dioxide.
CC -!- CATALYTIC ACTIVITY: CO + H(2)O + acceptor = CO(2) + reduced acceptor.
CC -!- COFACTOR: Molybdenum (molybdopterin).
CC -!- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND SMALL.
DR PIR; P0140; P0140.
KW Oxidoreductase; Molybdenum.
FT NON_TER 4
SQ SEQUENCE 4 AA; 441 MW; 7761E876F0000000 CRC64;

Query Match 28.6%; Score 6; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 G 2
DB 2 G 2

RESULT 4
EOSI_HUMAN STANDARD; PRT; 4 AA.
ID EOSI_HUMAN STANDARD; PRT; 4 AA.
AC P02731;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 01, Last annotation update)
DE Eosinophilotoxic peptides.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_SEQUENCE.
RP MEDLINE=76078412; PubMed=1060093;
RA Goetzl E.J., Austen K.F.;
RT "Purification and synthesis of eosinophilotoxic tetrapeptides of human lung tissue: identification as eosinophil chemotactic factor of anaphylaxis.";
RL Proc. Natl. Acad. Sci. U.S.A. 72:4123-4127(1975).
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CC -!- MISCELLANEOUS: These peptides are released from mast cells in lung (and other tissues) during hypersensitivity reactions (anaphylaxis). Their activities, preferentially affecting eosinophils, include chemotaxis, chemotactic deactivation, release of enzymes, and stimulation of the hexose monophosphate shunt.
DR GO:0008935; Pichemotaxis; IDA.
DR GO:0008955; P:Immune response; IDA.
FT VARIANT 1 V -> A (IN OTHER PEPTIDE).
FT SEQUENCE 4 AA; 390 MW; 6B05B862A0000000 CRC64;

Query Match 28.6%; Score 6; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 G 2
DB 2 G 2

RESULT 5
CCP3_OCTMI STANDARD; PRT; 4 AA.
ID CCP3_OCTMI STANDARD; PRT; 4 AA.
AC P58649;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cardioactive peptides Ocp-3/Ocp-4.
OS Octopus minor (Octopus).
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
OC Octopodiformes; Octopoda; Incirrata; Octopodidae; Octopus.
OX NCBI_TaxID=89766;
RN [1]_SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION.
RP TISSUE=Brain;
RC MEDLINE=20336815; PubMed=10876044;
RA Iwakoshi E., Hisada M., Minakata H.;
RT "Cardioactive peptides isolated from the brain of a Japanese octopus, Octopus minor.";
RL Peptides 21:623-630(2000).
CC -!- FUNCTION: Cardioactive; has both positive chronotropic and inotropic effects on the heart. Ocp-4 is a 1000 time less active than Ocp-3.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- PTM: Ocp-4 has D-Ser instead of L-Ser.
CC -!- MASS SPECTROMETRY: MW=395.2; METHOD=MALDI.
KW Hormone; D-amino acid.
FT MOD_RES 2 2 D-SERINE (IN OCP-4).
FT SEQUENCE 4 AA; 463 MW; 6AB365B810000000 CRC64;

Query Match 28.6%; Score 6; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 G 2
DB 1 G 1

RESULT 6
FAR3_HIRME STANDARD; PRT; 4 AA.
ID FAR3_HIRME STANDARD; PRT; 4 AA.
AC P42562;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE FMRFamide-like neuropeptide YLRP-amide.
OS Hirudo medicinalis (Medicinal leech).
OC Eukaryota; Metazoa; Annelida; Clitellata;
OC Arhynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
OX NCBI_TaxID=6421;
RN [1]_SEQUENCE.
```


RX MEDLINE=92195954; PubMed=1686933;
RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
RT "Identification of Rfamidae neuropeptides in the medicinal leech."
RL Peptides 12:897-908(1991).
CC -!- SIMILARITY: Belongs to the FARP (FMRPamide related peptide)
CC family.
KW Neuropeptide; Amidation.
FT MOD_RES 4 4
SQ SEQUENCE 4 AA; 598 MW; 69D4073B300000000 CRC64;

Query Match 23.8%; Score 5; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 R 1
Db 3 R 3

RESULT 7
FLRF_HIRME STANDARD; PRT; 4 AA.
ID FAR4_HIRME
AC P42563;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE FMRPamide-like neuropeptide YMRP-amide.
OS Hirudo medicinalis (Medicinal leech).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OC Arthropoda; Hirudiniiformes; Hirudinidae; Hirudo.
OX NCBI_TaxID=6421;
RN [1]
RP SEQUENCE.
RX MEDLINE=92195954; PubMed=1686933;
RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
RT "Identification of Rfamidae neuropeptides in the medicinal leech."
RL Peptides 12:897-908(1991).
CC -!- SIMILARITY: Belongs to the FARP (FMRPamide related peptide)
CC family.
KW Neuropeptide; Amidation.
FT MOD_RES 4 4
SQ SEQUENCE 4 AA; 616 MW; 69D4068B300000000 CRC64;

Query Match 23.8%; Score 5; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 R 1
Db 3 R 3

RESULT 8
FLRF_HIRME STANDARD; PRT; 4 AA.
ID FLRF_HIRME
AC P42561;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE FMRPamide.
OS Hirudo medicinalis (Medicinal leech), and
OS Helisoma trivolvis (Snail).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OC Arthropoda; Hirudiniiformes; Hirudinidae; Hirudo.
OX NCBI_TaxID=6421, 27815;
RN [1]
RP SEQUENCE.
RX MEDLINE=92195954; PubMed=1686933;
RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
RT "Identification of Rfamidae neuropeptides in the medicinal leech."
RL Peptides 12:897-908(1991).
RN [2]

RP SEQUENCE.
RX SPECIES=H. trivolvis; TISSUE=Kidney;
RC MEDLINE=94286417; PubMed=7912428;
RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;
RT "FMRPamide-related peptides from the kidney of the snail, Helisoma
trivolvis."
RL Peptides 15:31-36(1994).
CC -!- SIMILARITY: Belongs to the FARP (FMRPamide related peptide)
CC family.
KW Neuropeptide; Amidation.
FT MOD_RES 4 4
SQ SEQUENCE 4 AA; 582 MW; 69D40729A00000000 CRC64;

Query Match 23.8%; Score 5; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 R 1
Db 3 R 3

RESULT 9
FLRN_ATEL STANDARD; PRT; 4 AA.
ID FLRN_ATEL
AC P58707;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Antho-RNamide.
OS Anthopleura elegantissima (Sea anemone).
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
OC Nyantheae; Actiniidae; Anthopleura.
OX NCBI_TaxID=6110;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RX MEDLINE=90319122; PubMed=1973541;
RA Grimmelikhuijzen C.J.P., Rinehart K.L. Jr., Jacob E., Graff D.,
RA Reinscheid R.K., Nothacker H.-P., Staley A.L.;
RT "Isolation of L-3-phenylactyl-Leu-Arg-Asn-NH2 (Antho-RNamide), a sea
anemone neuropeptide containing an unusual amino-terminal blocking
group."
RL Proc. Natl. Acad. Sci. U.S.A. 87:5410-5414(1990).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Neuron specific.
CC -!- MASS SPECTROMETRY: MW=549.3; METHOD=FAB.
DR PIR; A35779; A35779.
KW Neuropeptide; Amidation.
FT MOD_RES 1 1
FT MOD_RES 4 4
SQ SEQUENCE 4 AA; 549 MW; 64540729A00000000 CRC64;

Query Match 23.8%; Score 5; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 R 1
Db 3 R 3

RESULT 10
FMRP_MACNI STANDARD; PRT; 4 AA.
ID FMRP_MACNI
AC P01162;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE FMRPamide (Peak C) (Cardioexcitatory neuropeptide).
OS Macrocaltista nimbosa (Sun-ray clam),
OS Nereis virens (Sandworm),
OS Hirudo medicinalis (Medicinal leech), and
OS Helisoma trivolvis (Snail).

OC Eukaryota; Metazoa; Mollusca; Bivalvia; Heteroconchia; Veneroidea;
 OC Veneroidea; Veneridae; Macrocallista.
 OX NCBI_TaxID=6594, 6353, 6421, 27815;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC SPECIES=M.nimbosa; TISSUE=Cerebral pedal, and Visceral ganglion;
 RX MEDLINE=77215956; PubMed=877582;
 RA Price D.A., Greenberg M.J.;
 RT "Structure of a molluscan cardioexcitatory neuropeptide";
 RL Science 197;670-671(1977).
 RN [2]
 RP SEQUENCE, AND CHARACTERIZATION.
 RC SPECIES=M.nimbosa; TISSUE=Ganglion;
 RX MEDLINE=78012038; PubMed=909875;
 RA Price D.A., Greenberg M.J.;
 RT "Purification and characterization of a cardioexcitatory neuropeptide
 from the central ganglia of a bivalve mollusc";
 RL Prep. Biochem. 7:261-281(1977).
 RN [3]
 RP SEQUENCE
 RC SPECIES=N.virens;
 RX MEDLINE=90259866; PubMed=23423992;
 RA Krajciak K.G., Price D.A.;
 RT "Authentic FMRFamide is present in the polychaete Nereis virens";
 RL Peptides 11:75-77(1990).
 RN [4]
 RP SEQUENCE
 RC SPECIES=H.medicinalis;
 RX MEDLINE=92195954; PubMed=1686933;
 RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
 RT "Identification of RFamide neuropeptides in the medicinal leech";
 RL Peptides 12:897-908(1991).
 RN [5]
 RP SEQUENCE
 RC SPECIES=H.trivolis; TISSUE=Kidney;
 RX MEDLINE=94286417; PubMed=7912428;
 RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;
 RT "FMRFamide-related peptides from the kidney of the snail, Helisoma
 trivolis";
 RL Peptides 15:31-36(1994).
 CC -!- FUNCTION: Myoactive; cardioexcitatory substance. Pharmacological
 activities include augmentation, induction, and regularization of
 cardiac contraction.
 CC -!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
 family.
 CC PIR; A01426; ECKN.
 DR PIR; A60418; A60418.
 KW Neuropeptide; Amidation.
 FT MOD RES 4
 SQ SEQUENCE 4 AA; 500 MW; 69D40699A0000000 CRC64;
 Query Match 23.8%; Score 5; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 R 1
 DB 3 R 3
 RESULT 11
 ID_FYRI ANTEL STANDARD; PRT; 4 AA.
 AC P58706;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Antho-Riamide I [Contains: Antho-Riamide II].
 OS Anthopleura elegantissima (Sea anemone).
 OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Anthopleura.
 OC Nynantheae; Actiniidae; Anthopleura.
 OX NCBI_TaxID=6110;
 RN [1]

RP SEQUENCE.
 RX MEDLINE=92270459; PubMed=1821096;
 RA Nothacker H.-P., Rinehart K.L. Jr., McFarlane I.D.,
 RA Grimmelikhuijzen C.J.P.;
 RT "Isolation of two novel neuropeptides from sea anemones: the unusual,
 biologically active L-3-phenyllactyl-Tyr-Arg-Ile-NH2 and its
 des-phenyllactyl fragment Tyr-Arg-Ile-NH2";
 RL Peptides 12:1165-1173(1991).
 RN [2]
 RP FUNCTION.
 RX MEDLINE=93391436; PubMed=8397415;
 RA McFarlane I.D., Hudman D., Nothacker H.-P., Grimmelikhuijzen C.J.P.;
 RT "The expansion behaviour of sea anemones may be coordinated by two
 inhibitory neuropeptides, Antho-Kamide and Antho-Riamide";
 RL Proc. R. Soc. Lond., B, Biol. Sci. 253:183-188(1993).
 CC -!- FUNCTION: Inhibits spontaneous contractions in several muscle
 groups. May be involved in the expansion phase of feeding
 behaviour in sea anemones.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Neuron specific.
 KW Neuropeptide; Amidation.
 FT CHAIN 1 4 ANTHO-RIAMIDE I.
 FT CHAIN 2 4 ANTHO-RIAMIDE II.
 FT MOD RES 1 1 L-3-PHENYLLACTYL.
 FT MOD RES 4 4 AMIDATION.
 SQ SEQUENCE 4 AA; 598 MW; 60441B59A0000000 CRC64;
 Query Match 23.8%; Score 5; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 R 1
 DB 3 R 3
 RESULT 12
 ID_TUFT HUMAN STANDARD; PRT; 4 AA.
 AC P01858;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Phagocytosis-stimulating peptide (Tuftsin).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=72187087; PubMed=4112769;
 RA Nishioka K., Constantopoulos A., Satoh P.S., Najjar V.A.;
 RT "The characteristics, isolation and synthesis of the phagocytosis
 stimulating peptide tuftsin";
 RL Biochem. Biophys. Res. Commun. 47:172-179(1972).
 RN [2]
 RP IMMUNOGLOBULIN CLASS.
 RX MEDLINE=68091045; PubMed=4169272;
 RA Fidalgo B.V., Najjar V.A.;
 RT "The physiological role of the lymphoid system. VI. The stimulatory
 effect of leucophilic gamma globulin (leucokinin) on the phagocytic
 activity of human polymorphonuclear leucocyte";
 RL Biochemistry 6:3386-3392(1967).
 CC -!- MISCELLANEOUS: An IgG (called leucokinin) binds reversibly to the
 cell membrane of neutrophils in the blood. Leucokininase on the
 membrane releases the active peptide tuftsin from the gamma chain.
 CC Tuftsin is essential for maximum stimulation of the phagocytic
 activity of neutrophils.
 CC PIR; A02147; A02147.
 DR MIM; 191150;
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006903; P:phagocytosis; NAS.
 SQ SEQUENCE 4 AA; 501 MW; 74176321C0000000 CRC64;

Query Match 23.8%; Score 5; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 R 1
 |
 4 R 4
 Db

RESULT 13
 DCMS_PSECH STANDARD; PRT; 4 AA.
 AC P19918;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Carbon monoxide dehydrogenase small chain (SC 1.2.99.2) (CO
 dehydrogenase subunit S) (CO-DH S) (Fragment).
 GN CUTS.
 OS Pseudomonas carboxydohydrogena.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Bradyrhizobiaceae.
 OX NCBI_TaxID=290;
 RN [1]
 RP SEQUENCE.

RX MEDLINE=90055678; PubMed=2818128;
 RA Kraut M., Hugendieck I., Herwig S., Meyer O.;
 RT "Homology and distribution of CO dehydrogenase structural genes in
 carboxydohydrogen bacteria";
 RL Arch. Microbiol. 152:335-341(1989).
 CC -!- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon
 dioxide.
 CC -!- CATALYTIC ACTIVITY: CO + H(2)O + acceptor = CO(2) + reduced
 acceptor.
 CC -!- COFACTOR: Binds 2 2Fe-2S clusters.
 CC -!- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
 SMALL.
 DR PIR; P19146; P19146.
 KW Oxidoreductase; Metal-binding; Iron-sulfur; Iron; 2Fe-2S.
 FT NON_TER 4
 SQ SEQUENCE 4 AA; 420 MW; 6DD33DD6F00000000 CRC64;

Query Match 19.0%; Score 4; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 A 4
 |
 2 A 2
 Db

RESULT 14
 PFKA_ANTL STANDARD; PRT; 4 AA.
 AC P56705;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Antho-KAamide.
 OS Anthopleura elegantissima (Sea anemone).
 OC Eukaryota; Metazoa; Chordata; Anthozoa; Zoantharia; Actiniaria;
 OC Nynanthaeae; Actiniidae; Anthopleura.
 OX NCBI_TaxID=6110;
 RN [1]
 RP SEQUENCE.

RX MEDLINE=92028852; PubMed=1681803;
 RA Nethacker H.-P., Rinehart K.L. Jr., Grimmelikhuijzen C.J.P.;
 RT "Isolation of L-3-phenyllactyl-Phe-Lys-Ala-NH2 (Antho-KAamide), a
 novel neuropeptide from sea anemones";
 RL Biochem. Biophys. Res. Commun. 179:1205-1211(1991).
 RN [2]
 RP FUNCTION.

RX MEDLINE=93391436; PubMed=8397415;
 RA McFarlane I.D., Hudman D., Nethacker H.-P., Grimmelikhuijzen C.J.P.;
 RT "The expansion behaviour of sea anemones may be coordinated by two
 inhibitory neuropeptides, Antho-KAamide and Antho-KIamide";
 RL Proc. R. Soc. Lond., B, Biol. Sci. 253:183-188(1993).
 CC -!- FUNCTION: Inhibits spontaneous contractions in several muscle
 groups. May be involved in the expansion phase of feeding
 behaviour in sea anemones.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Neuron specific.
 DR PIR; J01273; J01273.
 KW Neuropeptide; Amidation.
 FT MOD_RES 1 1 L-3-PHENYLLACTYL.
 FT MOD_RES 4 4 AMIDATION.
 SQ SEQUENCE 4 AA; 512 MW; 6DD339CA000000000 CRC64;

Query Match 19.0%; Score 4; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 A 4
 |
 4 A 4
 Db

RESULT 15
 RMOL_YEAST STANDARD; PRT; 4 AA.
 AC P36515;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-JUN-1994 (Rel. 29, Last annotation update)
 DE Mitochondrial 60S ribosomal protein L1 (Yml1) (Fragment).
 GN MRPL1.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE.

RX MEDLINE=91285106; PubMed=2060626;
 RA Grohmann L., Graack H.-R., Kruff V., Choli T., Goldschmidt-Reisin S.,
 RA Kitakawa M.;
 RT "Extended N-terminal sequencing of proteins of the large ribosomal
 subunit from yeast mitochondria";
 RL FEBS Lett. 284:51-56(1991).
 DR PIR; S17255; S17255.
 DR SGD; L002681; MRPL1.
 KW Ribosomal protein; Mitochondrion.
 FT NON_TER 4
 SQ SEQUENCE 4 AA; 402 MW; 7771B2D5D00000000 CRC64;

Query Match 4.8%; Score 1; DB 1; Length 4;
 Best Local Similarity 0.0%; Pred. No. 1.4e+05;
 Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 A 4
 |
 1 S 1
 Db

Search completed: February 26, 2004, 09:33:27
 Job time : 13 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 26, 2004, 09:30:35 ; Search time 39 Seconds
(without alignments)
32.361 Million cell updates/sec

Title: US-09-909-348-3

Perfect score: 21

Sequence: 1 RGDA 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 4

Maximum DB seq length: 4

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

SPREMBL 25: *
1: sp_archaea: *
2: sp_bacteria: *
3: sp_fungi: *
4: sp_human: *
5: sp_invertebrate: *
6: sp_mammal: *
7: sp_muc: *
8: sp_organelle: *
9: sp_phase: *
10: sp_plant: *
11: sp_rodent: *
12: sp_virus: *
13: sp_vertebrate: *
14: sp_unclassified: *
15: sp_rvirus: *
16: sp_bacteriap: *
17: sp_archaeap: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2	9.5	4	5	P83568 sepia offic
2	2	9.5	4	11	Q08433 rattus sp.

ALIGNMENTS

RESULT 1
P83568
ID P83568 PRELIMINARY; PRT; 4 AA.
AC P83568;
DT 01-JUN-2003 (TRENBLrel. 24, Created)
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Pheromone peptide ILME.
OS Sepia officinalis (Common cuttlefish).

OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neccoleoidea;
OC Decapodiformes; Sepioidae; Sepidae; Sepia.
OX NCBI_TaxID=6610;
RN [1]
RP SEQUENCE, SUBCELLULAR LOCATION, TISSUE SPECIFICITY, AND MASS
RP SPECTROMETRY.
RC TISSUE=EGG;
RX PubMed=10344467;
RA Zatylny C., Gagnon J., Boucaud-Camou E., Henry J.;
RT "ILME: a waterborne pheromonal peptide released by the eggs of Sepia
RT officinalis.";
RL Biochem. Biophys. Res. Commun. 275:217-222 (2000).
RN [2]
RP SEQUENCE.
RC TISSUE=EGG;
RX PubMed=12207899;
RA Zatylny C., Marvin L., Gagnon J., Henry J.;
RT "Fertilization in Sepia officinalis: the first mollusk sperm-
RT attracting peptide.";
RL Biochem. Biophys. Res. Commun. 296:1186-1193 (2002).
CC -!- FUNCTION: HAS MYOTROPIC ACTIVITY TARGETING THE GENITAL TRACT.
CC -!- SUBCELLULAR LOCATION: SECRETED.
CC -!- TISSUE SPECIFICITY: FOLLICLE, FULLY GROWN OOCYTE AND EGG (EC2).
CC -!- MASS SPECTROMETRY: MW=505.4; METHOD=MALDI.
DR GO: GO:0005186; F:pheromone activity; IEA.
KW Pheromone.
SQ SEQUENCE 4 AA; 505 MW; 6B16972030000000 CRC64;

Query Match 9.5%; Score 2; DB 5; Length 4;
Best Local Similarity 0.0%; Pred. No. 1e+06;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 D 3
DB 4 E 4

RESULT 2

Q08433
ID Q08433 PRELIMINARY; PRT; 4 AA.
AC Q08433;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Bilirubin UDP-glucuronosyltransferase (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Gunn;
RX MEDLINE=91282758; PubMed=1840486;
RA Sato H., Aono S., Kashiwamata S., Koizumi O.;
RT "Genetic defect of bilirubin UDP-glucuronosyltransferase in the
RT hyperbilirubinemic Gunn rat.";
RL Biochem. Biophys. Res. Commun. 177:1161-1164 (1991).
DR EMBL; S38636; AAB19259.1; -
DR GO: GO:0016740; F:transferase activity; IEA.
KW Transferase.
FT NON_TER 1
SQ SEQUENCE 4 AA; 473 MW; 633732C420000000 CRC64;

Query Match 9.5%; Score 2; DB 11; Length 4;
Best Local Similarity 0.0%; Pred. No. 1e+06;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 R 1
DB 4 K 4

Search completed: February 26, 2004, 09:34:18

Job time : 39 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 26, 2004, 09:24:10 ; Search time 52 Seconds
(without alignments)
21.734 Million cell updates/sec

Title: US-09-909-348-3

Perfect score: 21
Sequence: 1 RCDA 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 14389

Minimum DB seq length: 4
Maximum DB seq length: 4

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003s:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	100.0	4	AAR25315	Cell cont
2	21	100.0	4	AAB86859	Transport
3	21	100.0	4	AAE28333	Thrombo-s
4	21	100.0	4	AAU78374	Thrombin
5	21	100.0	4	AAE50856	Thrombin
6	21	100.0	4	AAE20157	Human thr
7	21	100.0	4	ADA44893	Human thr
8	21	100.0	4	ABB80263	Thrombin
9	18	85.7	4	AAE21325	Sequence
10	18	85.7	4	AAR34608	Antiviral
11	18	85.7	4	AAR26802	Iriglycer
12	18	85.7	4	AAR25312	Cell cont
13	18	85.7	4	AAR26810	Polyethyl
14	18	85.7	4	AAR26806	Propen-am
15	18	85.7	4	AAR26398	Sequence
16	18	85.7	4	AAR36713	Adhesion
17	18	85.7	4	AAR37833	Cell adhe
18	18	85.7	4	AAR44043	RGD pepti
19	18	85.7	4	AAR37134	RGD pepti
20	18	85.7	4	AAR37133	RGD pepti
21	18	85.7	4	AAR37137	RGD pepti
22	18	85.7	4	AAR37138	RGD pepti
23	18	85.7	4	AAR37132	RGD pepti
24	18	85.7	4	AAR37135	RGD pepti
25	18	85.7	4	AAR37130	RGD pepti

26	18	85.7	4	2	AAR37136	AAR37136 RGD pepti
27	18	85.7	4	2	AAR35464	AAR35464 Propepe-a
28	18	85.7	4	2	AAR44667	AAR44667 Platelet
29	18	85.7	4	2	AAR67015	AAR67015 RGD pepti
30	18	85.7	4	2	AAR57828	AAR57828 RGD contg
31	18	85.7	4	2	AAR53729	AAR53729 Tetrapept
32	18	85.7	4	2	AAR85667	AAR85667 Anti-alle
33	18	85.7	4	2	AAR62946	AAR62946 RGD contg
34	18	85.7	4	2	AAR70473	AAR70473 Cancer me
35	18	85.7	4	2	AAR29563	AAR29563 RGD pepti
36	18	85.7	4	2	ADD94859	ADD94859 Platelet
37	18	85.7	4	2	AAW11092	AAW11092 Platelet-
38	18	85.7	4	2	AAR98812	AAR98812 Cell adhe
39	18	85.7	4	2	AAW25174	AAW25174 RGD-pepti
40	18	85.7	4	2	AAW45489	AAW45489 Targeting
41	18	85.7	4	2	AAW45339	AAW45339 Peptide f
42	18	85.7	4	2	AAW35541	AAW35541 Peptide S
43	18	85.7	4	2	AAW31144	AAW31144 Platelet-
44	18	85.7	4	2	AAW62917	AAW62917 Part of t
45	18	85.7	4	2	AAW66842	AAW66842 Peptide u

ALIGNMENTS

RESULT 1
AAR25315
ID AAR25315 standard; peptide; 4 AA.
XX AAR25315;
XX AC
XX 17-MAR-1993 (first entry)
XX DT
XX DE Cell contact inhibitor generic peptide #4.
XX KW Cyclic peptide; cell contact inhibitor; hydrolytic enzyme.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Modified-site 2
XX PT /label= MeGly
XX PN JP04264097-A
XX PD 18-SEP-1992.
XX PF 16-FEB-1991; 91JP-00044386.
XX PR 16-FEB-1991; 91JP-00044386.
XX PA (ASAG) ASAHI GLASS CO LTD.
XX DR WPI; 1992-361922/44.
XX PT Peptide derivs. as contact inhibitor for animal cells - comprise
XX PT synthesised cyclic peptide and have portion of aminoacid sequence of
XX PT arginine-N-methyl:glycine-aspartic acid.
XX PS Disclosure; Page 3; 6pp; Japanese.
XX CC The sequences given in AAR25311-19 are cyclic peptides which act as
XX CC contact inhibitors of animal cells. They are resistant to decomposition
XX CC by hydrolytic enzymes and can be maintained at high levels of activity
XX CC for a long period in vivo. The peptides are cyclic and may have 1-16
XX CC pref. 1-4 amino acids
XX SQ Sequence 4 AA;

Query Match 100.0%; Score 21; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGDA 4
Db 1 RGDA 4

RESULT 2
AAB86859
ID AAB86859 standard; peptide; 4 AA.
XX AC AAB86859;
XX XX 28-NOV-2001 (first entry)
XX DE Transport molecule/ligand binding-associated peptide #5.
XX KW Transport molecule; ligand; cancer treatment; autoimmune disease;
XX KW inflammation; infection.
XX OS Synthetic.
XX XX WO200168142-A1.
XX XX 20-SEP-2001.
XX XX 13-MAR-2001; 2001WO-EP002833.
XX PR 13-MAR-2000; 2000DE-01012120.
XX PA (KTBT-) KTB TUMORFORSCHUNGS GMBH.
XX PI Kratz F;
XX DR WPI; 2001-589998/66.
XX XX New ligand, comprising therapeutic or diagnostic agent bonded non-covalently with substance having high affinity to transport molecule.
XX PS Disclosure; Page 39; 74pp; German.
XX XX This invention describes novel ligands which bind to transport molecules, comprising a therapeutic and/or diagnostic agent (A) non-covalently bonded via a linkage cleavable in vivo depending on pH and/or enzymatically with a substance (B) having an association constant KA to a transport molecule of above 10³ M⁻¹, is new. The medicaments are especially useful for the treatment of cancers, autoimmune diseases, acute and chronic inflammation and infections caused by viruses or microorganisms. The diagnostic kits are useful for the detection of these illnesses and for the detection of the transport molecule and/or its distribution in vivo. The ligands have excellent solubility in the medium at the site of action and are easy and inexpensive to convert into adducts, as the interaction with the transport material is physical.
XX CC AAB86843-AAB86920 represent peptides used to illustrate the method of the invention
XX SQ Sequence 4 AA;
Query Match 100.0%; Score 21; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGDA 4
Db 1 RGDA 4

RESULT 3
AAE28393
ID AAE28393 standard; peptide; 4 AA.
XX AC AAE28393;
XX XX 27-DEC-2002 (first entry)
XX DT
XX PI
XX XX

DE Thrombo-spondin 1 RGD cell binding region.
XX KW Tat region; nucleic acid-binding group; cell transfection system;
KW gene therapy; cancer; thrombo-spondin 1.
XX OS Unidentified.
XX XX US6376248-B1.
XX PN 23-APR-2002.
XX PD 16-MAR-1998; 98US-00039780.
XX PF 14-MAR-1997; 97US-00818200.
XX PR (LIFE-) LIFE TECHNOLOGIES INC.
XX PA Hawley-Nelson P, Lan J, Shih P, Jesse JA, Schifferli KP;
XX PI Gebeyehu G, Ciccarone VC, Evans KL;
XX DR WPI; 2002-680647/73.
XX XX New peptide comprising Tat sequence linked to nucleic acid-binding group, useful, e.g. in gene therapy, for improving cell-transfection efficiency.
XX PS Example 1; Col 65; 108pp; English.
XX XX The invention relates to a peptide comprising Tat sequence linked to nucleic acid-binding group. Peptides of the invention are used as components of a cell transfection system particularly for gene therapy (especially of cancer). The present sequence is thrombo-spondin 1 RGD cell binding region. This peptide is used in the exemplification of the invention
XX CC
XX SQ Sequence 4 AA;
Query Match 100.0%; Score 21; DB 5; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGDA 4
Db 1 RGDA 4

RESULT 4
AAU78374
ID AAU78374 standard; peptide; 4 AA.
XX AC AAU78374;
XX XX 18-JUN-2002 (first entry)
XX DT Thrombin peptide derivative #1.
XX DE Thrombin; osteopathic; receptor; agonist; bone growth stimulation; osteoinduction; farm animal; companion animal; laboratory animal; bone graft; segmental bone gap; bone void; non-union fracture.
XX OS Synthetic.
XX XX WO200205836-A2.
XX PN 24-JAN-2002.
XX XX 18-JUL-2001; 2001WO-US022641.
XX PF 19-JUL-2000; 2000US-0219300P.
XX PR (TEXA) UNIV TEXAS SYSTEM.
XX PA Carney DH, Crowther RS, Simmons DJ, Yang J, Redin WR;
XX PI
XX XX

DR WPI; 2002-303796/34.
 XX Stimulating bone growth at a site in a subject in need of osteoinduction,
 PT such as a site of bone graft, segmental bone gap, bone void or non-union
 PT structure, by administering agonist of activated thrombin receptor.
 XX
 PS Claim 9; Page 22; 27pp; English.
 XX
 CC The invention describes a method of stimulating bone growth at a site in
 CC a subject in need of osteoinduction. The method involves administering an
 CC agonist to stimulate bone growth at a site in a subject (e.g. a farm
 CC animal, companion animal or laboratory animal), in need of
 CC osteoinduction, such as the site in need of a bone graft in a subject, a
 CC segmental bone gap, a bone void or a non-union fracture. This sequence
 CC represents a thrombin peptide derivative obtained from a serine esterase
 CC that can stimulate or activate the non-proteolytically activated thrombin
 CC receptor
 XX
 SQ Sequence 4 AA;
 Query Match 100.0%; Score 21; DB 5; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RGDA 4
 Db ||||
 1 RGDA 4
 RESULT 5
 AAM50856
 ID AAM50856 standard; peptide; 4 AA.
 AC AAM50856;
 XX
 DT 01-MAY-2002 (first entry)
 XX
 DE Thrombin receptor binding domain used for cardiac tissue repair.
 XX
 KW Thrombin receptor binding domain; thrombin; revascularisation;
 KW vascular occlusion; tissue repair; vulnery; vasotropic; cardiant;
 KW angiogenesis; restenosis; therapy; human.
 XX
 OS Homo sapiens.
 XX
 PN WO200204008-A2.
 XX
 PD 17-JAN-2002.
 XX
 PF 12-JUL-2001; 2001WO-US021944.
 XX
 PR 12-JUL-2000; 2000US-0217583P.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 PI Carney DH;
 XX
 DR WPI; 2002-179665/23.
 XX
 PT Promoting cardiac tissue repair, stimulating revascularization,
 PT stimulating vascular endothelial cell proliferation, and inhibiting
 PT vascular occlusion by using angiogenic thrombin derivative peptide.
 XX
 PS Claim 2; Page 19; 24pp; English.
 XX
 CC The present sequence is that of a thrombin receptor binding domain
 CC peptide that is used in a claimed method for promoting cardiac tissue
 CC repair. The method involves administering an angiogenic thrombin-derived
 CC peptide. The peptide comprises the present thrombin receptor binding
 CC domain together with a serine esterase conserved sequence (see AAM50857),
 CC or preferably a peptide (see AAM50859) which includes both these
 CC sequences. The thrombin-derived peptide is administered during or
 CC following cardiac surgery by injection into cardiac tissue, and may be

CC formulated as a sustained release formulation. It is used in claimed
 CC methods of stimulating revascularisation, stimulating vascular
 CC endothelial cell proliferation, inhibiting vascular occlusion, and
 CC inhibiting restenosis following balloon angioplasty, in which case the
 CC peptide may be coated onto the catheter
 XX
 SQ Sequence 4 AA;
 Query Match 100.0%; Score 21; DB 5; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RGDA 4
 Db ||||
 1 RGDA 4
 RESULT 6
 AAE20157
 ID AAE20157 standard; peptide; 4 AA.
 XX
 AC AAE20157;
 XX
 DT 18-JUN-2002 (first entry)
 XX
 DE Human thrombin peptide.
 XX
 KW Cartilage growth; cartilage repair; arthritic joint; traumatic injury;
 KW non-proteolytically activated thrombin receptor; NPAR; chondrocyte;
 KW therapy; implantation; thrombin peptide; human.
 XX
 OS Homo sapiens.
 XX
 PN WO200207748-A2.
 XX
 PD 31-JAN-2002.
 XX
 PF 19-JUL-2001; 2001WO-US022668.
 XX
 PR 20-JUL-2000; 2000US-0219800P.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 PI Carney DH, Crowther RS, Stiernberg J, Bergmann J;
 XX
 DR WPI; 2002-268953/31.
 XX
 PT Stimulating growth and repair of cartilage, useful for treating e.g.
 PT arthritis, by local administration of an agonist of non-proteolytically
 PT activated thrombin receptor.
 XX
 PS Claim 10; Page 25; 28pp; English.
 XX
 CC The invention relates to a method of stimulating growth and repair of
 CC cartilage. The method involves administering to the site, an agonist of
 CC non-proteolytically activated thrombin receptor (NPAR). The method is
 CC used in human or veterinary medicine for the treatment of arthritic
 CC joints and damage/loss of cartilage caused by traumatic injury. Also
 CC chondrocytes may be cultured in presence of NPAR agonist to provide cells
 CC for implantation at sites requiring growth/repair of cartilage. The
 CC present sequence is human thrombin peptide. The derivatives of thrombin
 CC peptide which serves as a NPAR agonist
 XX
 SQ Sequence 4 AA;
 Query Match 100.0%; Score 21; DB 5; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RGDA 4
 Db ||||
 1 RGDA 4

RESULT 8
 ABB80263
 ID ABB80263 standard; peptide
 XX
 AC ABB80263;
 XX
 DT 18-DEC-2003 (first entry)

FT Misc-difference 4 /note= "attached to H or at least one AA"
FT PT /note= "attached to OH or at least one AA"
XX
PN US4614517-A.
XX
PD 30-SEP-1986.
XX
PF 17-JUN-1985; 85US-00745086.
XX
PR 04-AUG-1982; 82US-00405239.
PR 08-OCT-1982; 82US-00433457.
PR 28-JUL-1983; 83US-00518036.
XX 22-NOV-1983; 83US-00554821.
XX WPI; 1986-278506/42.
DR
XX
PS Claim 1; Col 8; 8pp; English.
XX
CC The patentors claim a compsn. which comprises AAP61325 is useful in
CC surgery and therapeutic reconstruction and treatment of injuries.
CC AAP61325 is the tetrapeptide sequence of fibronectin which promotes
CC attachment of suspended cells to tissue culture substrate as well as to
CC collagen, and is common to other proteins which interact with cells.
CC (Updated on 03-OCT-2002 to add missing OS field.)
XX
XX
SQ Sequence 4 AA;
Query Match 85.7%; Score 18; DB 1; Length 4;
Best Local Similarity 75.0%; Pred. No. 1.4e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 RGDA 4
DB 1 RGDS 4
RESULT 10
AAR04608
ID AAR04608 standard; protein; 4 AA.
XX
AC AAR04608;
XX
XX 25-MAR-2003 (revised)
DT 05-SEP-1990 (first entry)
XX
XX Antiviral agent.
XX Antiviral; M2; poliovirus; polio; hepatitis.
XX
XX Synthetic.
XX JP02078631-A.
XX
XX 19-MAR-1990.
XX
XX 14-SEP-1988; 88JP-00228843.
XX
XX 14-SEP-1988; 88JP-00228843.
XX (NIHA) NIPPON MINING CO.
XX WPI; 1990-129060/17.
XX
XX Antiviral agent contg. tri:peptide (unit) - of basic aminoacid, then
XX alanine, glycine or sarcosine, and acidic aminoacid, effective against
XX virus with protein-terminated DNA or RNA.
XX
XX Disclosure; Page ?; 4pp; Japanese.
XX
XX Peptide is effective against inhibiting propagation of DNA or RNA bonded,
XX protein containing viruses eg. Poliovirus, Hepatitis virus. (Updated on
XX 25-MAR-2003 to correct PA field.)
CC

XX
SQ Sequence 4 AA;
Query Match 85.7%; Score 18; DB 2; Length 4;
Best Local Similarity 75.0%; Pred. No. 1.4e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 RGDA 4
DB 1 RGDS 4
RESULT 11
AAR26802
ID AAR26802 standard; peptide; 4 AA.
XX
AC AAR26802;
XX
DT 11-FEB-1993 (first entry)
XX
XX Tri-glyceride-substituted peptide #1.
DE
XX Cell movement inhibitor; cell culture; adhesion membrane.
KW
XX Synthetic.
OS
XX
FH Key Location/Qualifiers
FT Modified-site 1
FT /note= "Arg is N-acetylated by the group; sn-CH2(OR1)-
FT CH(OR1)-CH2-O-CO(CH2)2-CO-Arg where R1= C16H33, n-C15H31
FT or 3,7,11,15-tetramethyl-hexadecyl"
XX
PN JP04208296-A.
XX
XX 29-JUL-1992.
PD
XX 30-NOV-1990; 90JP-00334794.
PF
XX 30-NOV-1990; 90JP-00334794.
PR
XX (FUJF) FUJI PHOTO FILM CO LTD.
PA
XX WPI; 1992-303598/37.
DR
XX Peptide deriv. - useful as cell movement inhibitor, cell adhesion
XX membrane or as culture substrate.
PT
XX Disclosure; Page 3; 8pp; Japanese.
PS
XX The sequences given in AAR26802-4 are examples of a highly generic
XX claimed peptide. These peptides are useful as cell movement inhibitors,
XX cell adhesion membranes and cell culture substrates
XX
SQ Sequence 4 AA;
Query Match 85.7%; Score 18; DB 2; Length 4;
Best Local Similarity 75.0%; Pred. No. 1.4e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 RGDA 4
DB 1 RGDS 4
RESULT 12
AAR25312
ID AAR25312 standard; peptide; 4 AA.
XX
AC AAR25312;
XX
XX 17-MAR-1993 (first entry)
DT
XX Cell contact inhibitor generic peptide #1.
CC

XX Cyclic peptide; cell contact inhibitor; hydrolytic enzyme.
 XX Synthetic.

XX Key Location/Qualifiers
 XX Modified-site 2 /label= MeGly

XX JP04264097-A.

XX 18-SEP-1992.

XX 16-FEB-1991; 91JP-00044386.

XX 16-FEB-1991; 91JP-00044386.

XX (ASAG) ASAHI GLASS CO LTD.

XX WPI; 1992-361922/44.

XX Peptide derivs. as contact inhibitor for animal cells - comprise
 XX synthesised cyclic peptide and have portion of aminoacid sequence of
 XX arginine-N-methyl:glycine-aspartic acid.

XX Disclosure; Page 3; 6pp; Japanese.

XX The sequences given in AAR25311-19 are cyclic peptides which act as
 XX contact inhibitors of animal cells. They are resistant to decomposition
 XX by hydrolytic enzymes and can be maintained at high levels of activity
 XX for a long period in vivo. The peptides are cyclic and may have 1-16
 XX pref. 1-4 amino acids

XX Sequence 4 AA;

Query Match 85.7%; Score 18; DB 2; Length 4;
 Best Local Similarity 75.0%; Pred. No. 1.4e+06;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGDA 4
 Db 1 RGDS 4

RESULT 13

AAR26810
 ID AAR26810 standard; peptide; 4 AA.

XX AAR26810;

XX 20-MAY-1998 (first entry)

XX Polyethylene glycol derivative #1.

XX triazine ring; methoxy-polyethylenoxy group; fibronectin; vitronectin;
 XX platelet adhesion; metastasis; neuropathy.

XX Synthetic.

XX JP04217693-A.

XX 07-AUG-1992.

XX 30-NOV-1990; 90JP-003333717.

XX 23-OCT-1990; 90JP-00285172.

XX (FUJIF) FUJII PHOTO FILM CO LTD.

XX WPI; 1992-312284/38.

XX Polyethylene glycol derivs. contg. peptide(s) - inhibit cellular adhesion
 XX for fibronectin or vitronectin and are used to inhibit agglutination or

PT adhesion of platelets.

XX Disclosure; Page 3; 9pp; Japanese.

XX The sequences given in AAR26810-14 are examples of a peptide chain which
 XX is attached once or twice to a triazine ring which is also substituted
 XX twice or once, respectively, with a methoxy-polyethylenoxy group. These
 XX peptides can be used to inhibit cellular adhesion to fibronectin or
 XX vitronectin and they are useful as inhibitors for agglutination or
 XX adhesion of platelets. They can also be useful as inhibitors for
 XX metastasis of cancers, inhibitors of agglutination of platelets caused by
 XX tumour cells in the blood capillaries, and drugs acting on neuropathy

XX Sequence 4 AA;

Query Match 85.7%; Score 18; DB 2; Length 4;
 Best Local Similarity 75.0%; Pred. No. 1.4e+06;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGDA 4

Db 1 RGDS 4

RESULT 14

AAR26806
 ID AAR26806 standard; peptide; 4 AA.

XX AAR26806;

XX 12-FEB-1993 (first entry)

XX Propen-amido peptide copolymer.

XX Tumour metastasis inhibitor; platelet aggregation; animal cell; adhesion;
 XX wound healing; cell culture media.

XX Synthetic.

Key Location/Qualifiers
 FT Modified-site 1
 FT /note= "CH2=CH-CO-NH-(CH2)3-CO-Arg"

XX JP04213311-A.

XX 04-AUG-1992.

XX 29-MAR-1991; 91JP-00066159.

XX 27-NOV-1990; 90JP-00324610.

XX (FUJIF) FUJII PHOTO FILM CO LTD.

XX WPI; 1992-305482/37.

XX New copolymers of propen-amido peptide(s) - are tumour metastasis,
 XX platelet aggregation and animal cell adhesion inhibitors also useful as
 XX wound healing agents and cell culture media.

XX Example; Page 6; 14pp; Japanese.

XX The sequence is that of a propen-amido peptide copolymer, it and its
 XX salts are water soluble and is useful as a tumour metastasis inhibitor, a
 XX platelet aggregation inhibitor, an animal cell adhesion inhibitor, a
 XX wound healing agent and cell culture media. See also AAR26805-R26808

XX Sequence 4 AA;

Query Match 85.7%; Score 18; DB 2; Length 4;
 Best Local Similarity 75.0%; Pred. No. 1.4e+06;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGDA 4

Db 1 RGDS 4
|||:
RESULT 15
AAR26398
ID AAR26398 standard; peptide; 4 AA.
XX AC AAR26398;
XX DT 25-MAR-2003 (revised)
DT 25-JAN-1993 (first entry)
XX DE Sequence of platelet binding peptide.
XX KW Technetium-99m labelled polypeptide imaging agent; radiolabeled imaging;
KW radiodiagnostic agent.
XX OS Synthetic.
XX PN WO9213572-A1.
XX PD 20-AUG-1992.
XX PF 07-FEB-1992; 92WO-US000757.
XX PR 08-FEB-1991; 91US-00653012.
XX PA (DIAT-) DIATECH INC.
XX PI Dean RT;
XX DR WPI; 1992-299767/36.
XX PT New technetium-99m labelled polypeptide imaging agents - for imaging of
PT clots, tumours, infection sites, atherosclerotic and amyloid plaques or
PT bone, and for visualising organs.
XX PS Claim 6; Page 13; 19pp; English.
XX CC The binding peptide is covalently linked to a 'Cp(aa)Cp' technetium
CC binding group wherein Cp is a protected cysteine and (aa) is an amino
CC acid. The technetium-99m complexes are used to image target sites within
CC a mammalian body. (Updated on 25-MAR-2003 to correct PN field.)
XX SQ Sequence 4 AA;
Query Match 85.7%; Score 18; DB 2; Length 4;
Best Local Similarity 75.0%; Pred. NO. 1.4e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RGDS 4
Db 1 RGDS 4
|||:
Search completed: February 26, 2004, 09:33:05
Job time : 54 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 26, 2004, 09:34:21 ; Search time 32 Seconds
(without alignments)
26.394 Million cell updates/sec

Title: US-09-909-348-3
Perfect score: 21
Sequence: 1 RGDA 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 809742 seqs, 21113259 residues

Total number of hits satisfying chosen parameters: 5110

Minimum DB seq length: 4
Maximum DB seq length: 4

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	21	100.0	4 9	US-09-909-348-3
2	21	100.0	4 9	US-09-904-090-1
3	21	100.0	4 9	US-09-909-122-3
4	21	100.0	4 10	US-09-911-569-23
5	21	100.0	4 13	US-10-050-692-3
6	21	100.0	4 13	US-10-050-611-1
7	21	100.0	4 13	US-10-050-688-3
8	21	100.0	4 14	US-10-200-879-23
9	18	85.7	4 9	US-09-823-444-6
10	18	85.7	4 9	US-09-010-714-9
11	18	85.7	4 9	US-09-925-715-21
12	18	85.7	4 9	US-03-935-168-1
13	18	85.7	4 9	US-09-942-117-5
14	18	85.7	4 10	US-09-911-569-22
15	18	85.7	4 11	US-09-991-588B-23

16	18	85.7	4 14	US-10-046-801-4	Sequence 4, Appli
17	18	85.7	4 14	US-10-215-435-5	Sequence 5, Appli
18	18	85.7	4 14	US-10-200-879-22	Sequence 22, Appl
19	18	85.7	4 14	US-10-021-660-130	Sequence 130, App
20	18	85.7	4 14	US-10-399-043-1	Sequence 1, Appli
21	18	85.7	4 14	US-10-300-694A-96	Sequence 96, Appli
22	18	85.7	4 14	US-10-405-339-60	Sequence 60, Appli
23	18	85.7	4 14	US-10-279-733-17	Sequence 17, Appli
24	18	85.7	4 15	US-10-297-229-39	Sequence 39, Appli
25	18	85.7	4 15	US-10-441-965-11	Sequence 11, Appli
26	18	85.7	4 16	US-10-208-894A-2	Sequence 2, Appli
27	17	81.0	4 9	US-09-892-071-4	Sequence 4, Appli
28	17	81.0	4 9	US-08-051-603-173	Sequence 173, Appl
29	17	81.0	4 9	US-08-051-603-175	Sequence 175, App
30	17	81.0	4 9	US-09-961-834-4	Sequence 4, Appli
31	17	81.0	4 9	US-09-961-834-5	Sequence 5, Appli
32	17	81.0	4 9	US-09-765-614B-1	Sequence 1, Appli
33	17	81.0	4 9	US-09-925-715-4	Sequence 4, Appli
34	17	81.0	4 9	US-09-972-772-32	Sequence 32, Appli
35	17	81.0	4 10	US-09-911-569-16	Sequence 16, Appli
36	17	81.0	4 10	US-09-911-569-18	Sequence 18, Appli
37	17	81.0	4 10	US-09-911-569-19	Sequence 19, Appli
38	17	81.0	4 10	US-09-911-569-20	Sequence 20, Appli
39	17	81.0	4 10	US-09-911-569-21	Sequence 21, Appli
40	17	81.0	4 11	US-09-991-588B-1	Sequence 1, Appli
41	17	81.0	4 11	US-09-991-588B-2	Sequence 2, Appli
42	17	81.0	4 13	US-10-001-945-32	Sequence 32, Appli
43	17	81.0	4 14	US-10-215-435-7	Sequence 7, Appli
44	17	81.0	4 14	US-10-215-435-10	Sequence 10, Appli
45	17	81.0	4 14	US-10-138-935-32	Sequence 32, Appli

ALIGNMENTS

RESULT 1
US-09-909-348-3
; Sequence 3, Application US/09909348
; Patent No. US20020042373A1
; GENERAL INFORMATION:
; APPLICANT: Garney, Darrell H.
; APPLICANT: Crowther, Roger S.
; APPLICANT: Stierberg, Janet
; APPLICANT: Bergmann, John
; TITLE OF INVENTION: Stimulation Of Cartilage Growth With Agonists
; TITLE OF INVENTION: Of The No. US20020042373A1-Proteolytically Activated Thrombin Rec
; FILE REFERENCE: 3033.1003-001
; CURRENT APPLICATION NUMBER: US/09/909,348
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/219,800
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 4
; TYPE: PXT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide fragment of Thrombin
US-09-909-348-3

Query Match 100.0%; Score 21; DB 9; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGDA 4
Db 1 RGDA 4

RESULT 2
US-09-904-090-1
; Sequence 1, Application US/09904090

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; Patent No. US20020061852A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; TITLE OF INVENTION: METHODS OF THERAPY WITH THROMBIN DERIVED
;   PEPTIDES
; FILE REFERENCE: 3033.1000-001
; CURRENT APPLICATION NUMBER: US/09/904,090
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: US 60/217,583
; PRIOR FILING DATE: 2000-07-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 4
;   TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide, fragment of thrombin
US-09-904-090-1

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Query Match      100.0%; Score 21; DB 9; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 RGDA 4
Db      1 RGDA 4

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RESULT 3
US-09-909-122-3
; Sequence 3, Application US/09909122
; Patent No. US20020128202A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; APPLICANT: Crowther, Roger S.
; APPLICANT: Simmons, David J.
; APPLICANT: Yang, Jinping
; APPLICANT: Redin, William R.
; TITLE OF INVENTION: Stimulation Of Bone Growth With Thrombin
;   DERIVATIVES
; FILE REFERENCE: 3033.1002-001
; CURRENT APPLICATION NUMBER: US/09/909,122
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/219,300
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 4
;   TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide fragment of Thrombin
US-09-909-122-3

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Query Match      100.0%; Score 21; DB 9; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 RGDA 4
Db      1 RGDA 4

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RESULT 4
US-09-911-569-23
; Sequence 23, Application US/09911569
; Publication No. US20030069173A1
; GENERAL INFORMATION:
; APPLICANT: HAWLEY-NELSON, PAMELA
; APPLICANT: LAN, JIANGQING
; APPLICANT: SHIH, POJEN

```

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; JESSE, JOEL A.
; SCHIFFERLI, KEVIN P.
; GEBEYEHU, GULILAT
; TITLE OF INVENTION: PEPTIDE-ENHANCED TRANSFECTIONS
; NUMBER OF SEQUENCES: 120
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GREENLEE, WINNER & SULLIVAN
; STREET: 5370 MANHATTAN CIRCLE, SUITE 201
; CITY: BOULDER
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/911,569
; FILING DATE: 23-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/039,780
; FILING DATE: 16-MAR-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: SULLIVAN, SALLY A.
; REGISTRATION NUMBER: 32,064
; REFERENCE/DOCKET NUMBER: 32-95D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303)499-8080
; TELEFAX: (303)499-8089
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 4 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: not relevant
;   TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-911-569-23

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Query Match      100.0%; Score 21; DB 10; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 RGDA 4
Db      1 RGDA 4

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RESULT 5
US-10-050-692-3
; Sequence 3, Application US/10050692
; Publication No. US20020182205A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; APPLICANT: Crowther, Roger S.
; APPLICANT: Simmons, David J.
; APPLICANT: Yang, Jinping
; APPLICANT: Redin, William R.
; TITLE OF INVENTION: STIMULATION OF BONE GROWTH WITH THROMBIN
;   DERIVATIVES
; FILE REFERENCE: 3033.1002-004
; CURRENT APPLICATION NUMBER: US/10/050,692
; CURRENT FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: 09/909,122
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/219,300
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0

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; SEQ ID NO 3
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fragment of human prothrombin
US-10-050-692-3

Query Match      100.0%; Score 21; DB 13; Length 4;
Best Local Similarity 100.0%; Pred. NO. 7.2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RGDA 4
Db      1 RGDA 4

RESULT 6
US-10-050-611-1
; Sequence 1, Application US/10050611
; Publication No. US2002018793A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; TITLE OF INVENTION: METHODS OF THERAPY WITH THROMBIN DERIVED
; TITLE OF INVENTION: PEPTIDES
; FILE REFERENCE: 3033.1000-008
; CURRENT APPLICATION NUMBER: US/10/050,611
; CURRENT FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: 09/904,090
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 60/217,583
; PRIOR FILING DATE: 2000-07-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human fragment of thrombin
US-10-050-611-1

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Best Local Similarity 100.0%; Pred. NO. 7.2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RGDA 4
Db      1 RGDA 4

RESULT 7
US-10-050-688-3
; Sequence 3, Application US/10050688
; Publication No. US20020198154A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; APPLICANT: Crowther, Roger S.
; APPLICANT: Stierberg, Janet
; APPLICANT: Bergmann, John
; TITLE OF INVENTION: STIMULATION OF CARTILAGE GROWTH WITH
; TITLE OF INVENTION: AGONISTS OF THE NON-PROTEOLYTICALLY ACTIVATED THROMBIN
; TITLE OF INVENTION: RECEPTOR
; FILE REFERENCE: 3033.1003-004
; CURRENT APPLICATION NUMBER: US/10/050,688
; CURRENT FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: 09/909,348
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/219,800
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3

; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide fragment of thrombin
US-10-050-688-3

Query Match      100.0%; Score 21; DB 13; Length 4;
Best Local Similarity 100.0%; Pred. NO. 7.2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RGDA 4
Db      1 RGDA 4

RESULT 8
US-10-200-879-23
; Sequence 23, Application US/10200879
; Publication No. US20030144230A1
; GENERAL INFORMATION:
; APPLICANT: HAWLEY-NELSON, PAMELA
; APPLICANT: LAN, JIANQING
; APPLICANT: SHIH, POEEN
; APPLICANT: JESSE, JOEL A.
; APPLICANT: SCHIFFERLI, KEVIN P.
; APPLICANT: GEBYEHEU, GULILAT
; TITLE OF INVENTION: PEPTIDE-ENHANCED TRANSECTIONS
; NUMBER OF SEQUENCES: 120
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GREENLEE, WINNER & SULLIVAN
; STREET: 5370 MANHATTAN CIRCLE, SUITE 201
; CITY: BOULDER
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/200,879
; FILING DATE: 23-Jul-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/911,569
; FILING DATE: 23-JUL-2001
; APPLICATION NUMBER: US 09/039,780
; FILING DATE: 16-MAR-1998
; APPLICATION NUMBER: US 08/818,200
; FILING DATE: 14-MAR-1997
; APPLICATION NUMBER: US 08/658,130
; FILING DATE: 04-JUN-1996
; APPLICATION NUMBER: US 08/477,354
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: SULLIVAN, SALLY A.
; REGISTRATION NUMBER: 32,064
; REFERENCE/DOCKET NUMBER: 32-95E
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303)499-8080
; TELEFAX: (303)499-8089
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
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US-10-200-879-23
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Best Local Similarity 100.0%; Pred. No. 7.2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RGDA 4
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Db      1 RGDA 4

RESULT 9
US-09-823-444-6
; Sequence 6, Application US/09823444
; Patent No. US20020009753A1
; GENERAL INFORMATION:
; APPLICANT: Bednar, Bohumil
; APPLICANT: Bollag, Daniel M.
; APPLICANT: Gould, Robert J.
; APPLICANT: Merck & Co., Inc.
; TITLE OF INVENTION: ANTICOAGULANT TEST
; FILE REFERENCE: 19910
; CURRENT APPLICATION NUMBER: US/09/823,444
; CURRENT FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: This sequence is a synthetically prepared peptide.
US-09-823-444-6

Query Match      85.7%; Score 18; DB 9; Length 4;
Best Local Similarity 75.0%; Pred. No. 7.2e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 RGDA 4
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Db      1 RGDS 4

RESULT 10
US-09-010-714-9
; Sequence 9, Application US/09010714
; Patent No. US20020012942A1
; GENERAL INFORMATION:
; APPLICANT: McCarthy, James B.
; APPLICANT: Furcht, Leo T.
; APPLICANT: Iida, Joji
; TITLE OF INVENTION: POLYPEPTIDES WITH ALPHA 4 INTEGRIN SUBUNIT RELATED
; FILE REFERENCE: 600.332US01
; CURRENT APPLICATION NUMBER: US/09/010,714
; CURRENT FILING DATE: 1998-01-22
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-010-714-9

Query Match      85.7%; Score 18; DB 9; Length 4;
Best Local Similarity 75.0%; Pred. No. 7.2e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 RGDA 4
      ||||
Db      1 RGDS 4

US-10-200-879-23
Query Match      100.0%; Score 21; DB 14; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RGDA 4
      ||||
Db      1 RGDA 4

RESULT 9
US-09-823-444-6
; Sequence 6, Application US/09823444
; Patent No. US20020009753A1
; GENERAL INFORMATION:
; APPLICANT: Bednar, Bohumil
; APPLICANT: Bollag, Daniel M.
; APPLICANT: Gould, Robert J.
; APPLICANT: Merck & Co., Inc.
; TITLE OF INVENTION: ANTICOAGULANT TEST
; FILE REFERENCE: 19910
; CURRENT APPLICATION NUMBER: US/09/823,444
; CURRENT FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: This sequence is a synthetically prepared peptide.
US-09-823-444-6

Query Match      85.7%; Score 18; DB 9; Length 4;
Best Local Similarity 75.0%; Pred. No. 7.2e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 RGDA 4
      ||||
Db      1 RGDS 4

RESULT 10
US-09-010-714-9
; Sequence 9, Application US/09010714
; Patent No. US20020012942A1
; GENERAL INFORMATION:
; APPLICANT: McCarthy, James B.
; APPLICANT: Furcht, Leo T.
; APPLICANT: Iida, Joji
; TITLE OF INVENTION: POLYPEPTIDES WITH ALPHA 4 INTEGRIN SUBUNIT RELATED
; FILE REFERENCE: 600.332US01
; CURRENT APPLICATION NUMBER: US/09/010,714
; CURRENT FILING DATE: 1998-01-22
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-010-714-9

Query Match      85.7%; Score 18; DB 9; Length 4;
Best Local Similarity 75.0%; Pred. No. 7.2e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 RGDA 4
      ||||
Db      1 RGDS 4

US-09-925-715-21
RESULT 11
US-09-925-715-21
; Sequence 21, Application US/09925715
; Patent No. US20020102217A1
; GENERAL INFORMATION:
; APPLICANT: NYcomed Imaging AS
; TITLE OF INVENTION: Improvements in or relating to diagnostic/therapeutic
; FILE REFERENCE: REF/Klavness/206
; CURRENT APPLICATION NUMBER: US/09/925,715
; CURRENT FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic RGDS
; OTHER INFORMATION: sequence
US-09-925-715-21

Query Match      85.7%; Score 18; DB 9; Length 4;
Best Local Similarity 75.0%; Pred. No. 7.2e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 RGDA 4
      ||||
Db      1 RGDS 4

RESULT 12
US-09-935-168-1
; Sequence 1, Application US/09935168
; Patent No. US20020106793A1
; GENERAL INFORMATION:
; APPLICANT: West, Jennifer L.
; APPLICANT: Mann, Brenda K.
; TITLE OF INVENTION: Issue Engineering Scaffolds Promoting Matrix Protein Production
; FILE REFERENCE: RICE 103
; CURRENT APPLICATION NUMBER: US/09/935,168
; CURRENT FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: cell adhesion ligand
US-09-935-168-1

Query Match      85.7%; Score 18; DB 9; Length 4;
Best Local Similarity 75.0%; Pred. No. 7.2e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 RGDA 4
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Db      1 RGDS 4

RESULT 13
US-09-942-117-5
; Sequence 5, Application US/09942117
; Publication No. US20020197700A1
; GENERAL INFORMATION:
; APPLICANT: MENRAD, ANDREAS
; APPLICANT: REDLITZ, ALEXANDER
; APPLICANT: KOPPLITZ, MARCUS
; APPLICANT: EGNER, URSULA
; APPLICANT: BAHR, INKE
; TITLE OF INVENTION: RECEPTOR OF THE EDB-FIBRONECTIN DOMAINS
; FILE REFERENCE: SCH-1832
US-09-942-117-5

Query Match      85.7%; Score 18; DB 9; Length 4;
Best Local Similarity 75.0%; Pred. No. 7.2e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 RGDA 4
      ||||
Db      1 RGDS 4

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; CURRENT APPLICATION NUMBER: US/09/942,117
; CURRENT FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: DE 10045803.3
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: DE 10123133.4-41
; PRIOR FILING DATE: 2001-05-20
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-942-117-5

Query Match 85.7%; Score 18; DB 9; Length 4;
Best Local Similarity 75.0%; Pred. No. 7.2e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGDA 4
Db 1 RGDS 4

RESULT 14
US-09-911-569-22
; Sequence 22, Application US/09911569
; Publication No. US20030069173A1
; GENERAL INFORMATION:
; APPLICANT: HAWLEY-NELSON, PAMELA
; LAN, JIANQING
; SHIR, POJEN
; JESSE, JOEL A.
; SCHIFFERLI, KEVIN P.
; GEBVEHU, GULILAT
; TITLE OF INVENTION: PEPTIDE-ENHANCED TRANSFECTIONS
; NUMBER OF SEQUENCES: 120
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GREENLEE, WINNER & SULLIVAN
; STREET: 5370 MANHATTAN CIRCLE, SUITE 201
; CITY: BOULDER
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/911,569
; FILING DATE: 23-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/039,780
; FILING DATE: 16-MAR-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: SULLIVAN, SALLY A.
; REGISTRATION NUMBER: 32,064
; REFERENCE/DOCKET NUMBER: 32-95D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303)499-8080
; TELEFAX: (303)499-8089
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO

; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-911-589-22

Query Match 85.7%; Score 18; DB 10; Length 4;
Best Local Similarity 75.0%; Pred. No. 7.2e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGDA 4
Db 1 RGDS 4

RESULT 15
US-09-991-588B-23
; Sequence 23, Application US/09991588B
; Publication No. US20030219429A1
; GENERAL INFORMATION:
; APPLICANT: Budny, John A.
; TITLE OF INVENTION: Compositionand Method for Bone Regeneration
; FILE REFERENCE: 1008-120.US
; CURRENT APPLICATION NUMBER: US/09/991,588B
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 09/122,348
; PRIOR FILING DATE: 1998-07-24
; NUMBER OF SEQ ID NOS: 23
; SEQ ID NO 23
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Purchased commercially or sequence is synthesized
US-09-991-588B-23

Query Match 85.7%; Score 18; DB 11; Length 4;
Best Local Similarity 75.0%; Pred. No. 7.2e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGDA 4
Db 1 RGDS 4

Search completed: February 26, 2004, 09:39:36
Job time : 33 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 26, 2004, 09:32:06 ; Search time 23 Seconds
(without alignments)
8.978 Million cell updates/sec

Title: US-09-909-348-3
Perfect score: 21
Sequence: 1 RGDA 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 9930

Minimum DB seq length: 4
Maximum DB seq length: 4

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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4: /cgn2_6/prodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/prodata/2/iaa/PGTUS_COMB.pep.*
6: /cgn2_6/prodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	4	1	US-08-658-130-19
2	21	100.0	4	4	US-09-039-780A-23
3	21	100.0	4	4	US-08-538-504-1
4	21	100.0	4	4	US-09-631-137C-1
5	21	100.0	4	5	FCI-US96-08723-19
6	21	100.0	4	6	5352664-2
7	18	85.7	4	1	US-07-780-790A-7
8	18	85.7	4	1	US-07-683-957B-7
9	18	85.7	4	1	US-07-834-848-16
10	18	85.7	4	1	US-08-127-351-54
11	18	85.7	4	1	US-08-109-106-1
12	18	85.7	4	1	US-08-251-027-8
13	18	85.7	4	1	US-08-480-367B-54
14	18	85.7	4	1	US-08-487-221A-54
15	18	85.7	4	1	US-08-480-370-54
16	18	85.7	4	1	US-08-389-005-1
17	18	85.7	4	1	US-08-178-482-11
18	18	85.7	4	1	US-08-299-636-35
19	18	85.7	4	1	US-08-279-155-34
20	18	85.7	4	1	US-08-142-449B-13
21	18	85.7	4	1	US-08-464-456-33
22	18	85.7	4	1	US-08-128-225-2
23	18	85.7	4	1	US-08-405-200-1
24	18	85.7	4	1	US-08-596-116A-67
25	18	85.7	4	1	US-08-596-116A-70
26	18	85.7	4	1	US-08-338-282-12
27	18	85.7	4	1	US-08-658-130-18

Sequence 108, Appl
Sequence 28, Appl
Sequence 1, Appl
Sequence 55, Appl
Sequence 28, Appl
Sequence 34, Appl
Sequence 33, Appl
Sequence 28, Appl
Sequence 13, Appl
Sequence 33, Appl
Sequence 1, Appl
Sequence 14, Appl
Sequence 28, Appl
Sequence 1, Appl
Sequence 6, Appl
Sequence 25, Appl

18 85.7 4 1 US-08-462-661A-108
18 85.7 4 1 US-08-421-702A-28
30 18 85.7 4 1 US-08-343-264-1
31 18 85.7 4 1 US-08-487-568-55
32 18 85.7 4 1 US-08-421-696A-28
33 18 85.7 4 1 US-08-703-988A-34
34 18 85.7 4 1 US-08-483-052-33
35 18 85.7 4 1 US-08-421-697A-28
36 18 85.7 4 1 US-08-421-698A-28
37 18 85.7 4 2 US-08-668-871-13
38 18 85.7 4 2 US-08-480-551-33
39 18 85.7 4 2 US-08-669-683-13
40 18 85.7 4 2 US-08-836-854-1
41 18 85.7 4 2 US-08-480-133A-14
42 18 85.7 4 2 US-08-421-695A-28
43 18 85.7 4 2 US-08-807-464-1
44 18 85.7 4 2 US-08-934-222-6
45 18 85.7 4 2 US-08-747-137-25

ALIGNMENTS

RESULT 1
US-08-658-130-19
; Sequence 19, Application US/08658130
; Patent No. 5736392
; GENERAL INFORMATION:
; APPLICANT: Hawley-Nelson, Pamela
; APPLICANT: Lan, Jiangling
; APPLICANT: Shih, Pojen
; APPLICANT: Jesse, Joel A.
; APPLICANT: Shifferli, Kevin P.
; TITLE OF INVENTION: Peptide-Enhanced Cationic Lipid
; TITLE OF INVENTION: Transfections
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: Colorado
; COUNTRY: US
; ZIP: 80303

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/658,130
FILING DATE: 04-JUN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/477,354
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Caruthers, Jennie M.
REGISTRATION NUMBER: 34,464
REFERENCE/DOCKET NUMBER: 32-95A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO.: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
US-08-658-130-19

Query Match 100.0%; Score 21; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGDA 4
Db 1 RGDA 4

RESULT 2
US-09-039-780A-23
; Sequence 23, Application US/09039780A
; Patent No. 6376248
; GENERAL INFORMATION:
; APPLICANT: HAWLEY-NEILSON, PAMELA
; LAN, JIANQING
; SHIH, FOJEN
; JESSE, JOEL A.
; SCHIFFERLI, KEVIN P.
; GEBREYEHU, GULILAT
; TITLE OF INVENTION: PEPTIDE-ENHANCED TRANSFECTIONS
; NUMBER OF SEQUENCES: 120
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GREENLEE, WINNER & SULLIVAN
; STREET: 5370 MANHATTAN CIRCLE, SUITE 201
; CITY: BOULDER
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/039,780A
; FILING DATE: 16-Mar-1998
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: SULLIVAN, SALLY A.
; REGISTRATION NUMBER: 32,064
; REFERENCE/DOCKET NUMBER: 32-95C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303)499-8089
; TELEFAX: (303)499-8089
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-039-780A-23

Query Match 100.0%; Score 21; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGDA 4
Db 1 RGDA 4

RESULT 3
US-08-538-504-1
; Sequence 1, Application US/08538504
; Patent No. 6627731
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; APPLICANT: Glenn, Kevin C.

; TITLE OF INVENTION: THROMBIN DERIVED POLYPEPTIDES:
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/538,504
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, David L.
; REGISTRATION NUMBER: 32,165
; REFERENCE/DOCKET NUMBER: UTSG:178/PAR
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-538-504-1

Query Match 100.0%; Score 21; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGDA 4
Db 1 RGDA 4

RESULT 4
US-09-631-137C-1
; Sequence 1, Application US/09631137C
; Patent No. 6630572
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; APPLICANT: Glenn, Kevin C.
; TITLE OF INVENTION: Thrombin Derived Polypeptides:
; TITLE OF INVENTION: Compositions and Methods for Use
; FILE REFERENCE: 3033.1001-004
; CURRENT APPLICATION NUMBER: US/09/631,137C
; CURRENT FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 08/538,504
; PRIOR FILING DATE: 1995-09-29
; PRIOR APPLICATION NUMBER: US 08/007,173
; PRIOR FILING DATE: 1993-01-21
; PRIOR APPLICATION NUMBER: US 06/925,201
; PRIOR FILING DATE: 1986-10-31
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fragment of human prothrombin
US-09-631-137C-1

Query Match 100.0%; Score 21; DB 4; Length 4;

Best Local Similarity 100.0%; Pred. No. 3e+05; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0;

QY 1 RGDA 4
Db 1 RGDA 4

RESULT 5
PCT-US96-08723-19
; Sequence 19, Application PC/TUS9608723
; GENERAL INFORMATION:
; APPLICANT: Life Technologies, Inc.
; TITLE OF INVENTION: Peptide-Enhanced Cationic Lipid
; TITLE OF INVENTION: Transfections
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: Colorado
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/08723
; FILING DATE: 04-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/477,354
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Caruthers, Jennie M.
; REGISTRATION NUMBER: 34,464
; REFERENCE/DOCKET NUMBER: 3295A WO
; TELEPHONE: (303) 499-8080
; TELEFAX: (303) 499-8089
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE: internal
; PCT-US96-08723-19

Query Match 100.0%; Score 21; DB 5; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGDA 4
Db 1 RGDA 4

RESULT 6
5352664-2
; Patent No. 5352664
; APPLICANT: Carney, Darrell H.; Glenn, Kevin C.
; TITLE OF INVENTION: THROMBIN DERIVED POLYPEPTIDES
; COMPOSITIONS AND METHODS FOR USE
; NUMBER OF SEQUENCES: 3
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/925,201
; FILING DATE: 31-OCT-1996
; SEQ ID NO: 2:

LENGTH: 4
5352664-2

Query Match 100.0%; Score 21; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGDA 4
Db 1 RGDA 4

RESULT 7
US-07-780-790A-7
; Sequence 7, Application US/07780790A
; Patent No. 5238488
; GENERAL INFORMATION:
; APPLICANT: KOJIMA, Masayoshi
; APPLICANT: KOMAZAWA, Hiroyuki
; TITLE OF INVENTION: CM-CHITIN DERIVATIVES AND USE THEREOF
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sughrue, Mion, Zinn, Macpeak, & Seas
; STREET: 2100 Pennsylvania Avenue
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/780,790A
; FILING DATE: 19911023
; CLASSIFICATION: 530
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)293-7060
; TELEFAX: (202)293-7860
; TELEX: 6491103
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-07-780-790A-7

Query Match 85.7%; Score 18; DB 1; Length 4;
Best Local Similarity 75.0%; Pred. No. 3e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGDA 4
Db 1 RGDS 4

RESULT 8
US-07-683-957B-7
; Sequence 7, Application US/07683957B
; Patent No. 531880
; GENERAL INFORMATION:
; APPLICANT: Donahoe, Patricia K.
; APPLICANT: Ragin, Richard C.
; APPLICANT: MacLaughlin, David T.
; TITLE OF INVENTION: Purification of M llerian Inhibiting
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington

```

; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: /07/683,957B
; APPLICATION NUMBER: US/07/683,957B
; FILING DATE: 19910412
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldstein, Jorge A.
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 0609,3060000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 466-0800
; TELEFAX: (202) 933-8716
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-683-957B-7

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Query Match 85.7%; Score 18; DB 1; Length 4;
 Best Local Similarity 75.0%; Pred. No. 3e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0;

QY 1 RGDA 4
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 DB 1 RGDS 4

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RESULT 9
US-07-834-848-16
; Sequence 16, Application US/07834848
; Patent No. 5436221
; GENERAL INFORMATION:
; APPLICANT: KITAGUCHI, HIROSHI
; APPLICANT: KOMAZAWA, HIROYUKI
; APPLICANT: KOJIMA, MASAYOSHI
; APPLICANT: MORI, HIDEKO
; APPLICANT: NISHIKAWA, NAOTYUKI
; APPLICANT: SATOH, HIDEAKI
; APPLICANT: ORIKASA, ATSUSHI
; APPLICANT: ONO, MITSUNORI
; APPLICANT: AZUMA, ICHIRO
; APPLICANT: SAIKI, IKUO
; TITLE OF INVENTION: PEPTIDE DERIVATIVES AND APPLICATION
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sughrue, Mion, Zinn, Macpeak, & Seas
; STREET: 2100 Pennsylvania Ave., NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20037-3202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/834,848
; FILING DATE: 19920213
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Biggart, Waddell A.
; REGISTRATION NUMBER: 24,861

```

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; REFERENCE/DOCKET NUMBER: Q28480
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)293-7060
; TELEFAX: (202)293-7860
; TELEX: 6491103
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-07-834-848-16

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Query Match 85.7%; Score 18; DB 1; Length 4;
 Best Local Similarity 75.0%; Pred. No. 3e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0;

QY 1 RGDA 4
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 DB 1 RGDS 4

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RESULT 10
US-08-127-351-54
; Sequence 54, Application US/08127351
; Patent No. 5449761
; GENERAL INFORMATION:
; APPLICANT: BELINKA Jr, BENJAMIN A.
; APPLICANT: COUGHLIN, DANIEL J.
; APPLICANT: ALVAREZ, VERNON L.
; APPLICANT: WOOD, RICHARD
; TITLE OF INVENTION: METAL-BINDING TARGETED POLYPEPTIDE
; TITLE OF INVENTION: CONSTRUCTS
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER &
; ADDRESSEE: NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1765 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/127,351
; FILING DATE: 28-SEP-1993
; CLASSIFICATION: 534
; ATTORNEY/AGENT INFORMATION:
; NAME: Villacorta, Gilberto M.
; REGISTRATION NUMBER: 34,038
; REFERENCE/DOCKET NUMBER: 4980-004-44
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-127-351-54

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Query Match 85.7%; Score 18; DB 1; Length 4;
 Best Local Similarity 75.0%; Pred. No. 3e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0;

QY 1 RGDA 4

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DB      1 RGDS 4
;
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
;
; US-08-109-106-1
;
; Query Match      85.7%; Score 18; DB 1; Length 4;
; Best Local Similarity 75.0%; Pred. No. 3e+05;
; Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
;
; QY      1 RGDA 4
;         |||:
; DB      1 RGDS 4
;
; RESULT 12
; US-08-251-027-8
; Sequence 8, Application US/08251027
; Patent No. 5519005
; GENERAL INFORMATION:
; APPLICANT: Lider, Ofer
; APPLICANT: Greenspoon, No. 5519005m
; APPLICANT: Herskowitz, Rami
; APPLICANT: Alon, Ronen
; TITLE OF INVENTION: A METHOD OF INHIBITION OF CELLULAR AND
; TITLE OF INVENTION: MOLECULAR LEVEL BIOLOGICAL INTERACTIONS UTILIZING
; TITLE OF INVENTION: NON-PEPTIDIC SURROGATES OF THE ARG-GLY-ASP SEQUENCE
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kohn & Associates
; STREET: 30500 No. 5519005thwestern Highway, Suite 410
; CITY: Farmington Hills
; STATE: Michigan
; COUNTRY: U.S.
; ZIP: 48334
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/251.027
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohn, Kenneth I.
; REGISTRATION NUMBER: 30,955
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (810) 539-5050
; TELEFAX: (810) 539-5055
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-251-027-8
;
; Query Match      85.7%; Score 18; DB 1; Length 4;
; Best Local Similarity 75.0%; Pred. No. 3e+05;
; Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
;
; QY      1 RGDA 4
;         |||:
; DB      1 RGDS 4
;
; RESULT 11
; US-08-109-106-1
; Sequence 1, Application US/08109106
; Patent No. 5475100
; GENERAL INFORMATION:
; APPLICANT: Kimikazu HASHINO et al.
; TITLE OF INVENTION: Artificial Antibody
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: DisplayWrite
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/109.106
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION NUMBER: 07/725,668
; FILING DATE: July 3, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX: 202-371-8856
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE:
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
; PUBLICATION INFORMATION:
; AUTHORS:

```

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RESULT 13
US-08-480-367B-54
; Sequence 54, Application US/08480367B
; Patent No. 5578298
; GENERAL INFORMATION:
; APPLICANT: BELINKA JR, BENJAMIN A.
; APPLICANT: COUGHLIN, DANIEL J.
; APPLICANT: ALVAREZ, VERNON L.
; APPLICANT: WOOD, RICHARD
; TITLE OF INVENTION: METAL-BINDING TARGETED POLYPEPTIDE
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LOWE, PRICE, LeBLANC & BECKER
; STREET: 99 Canal Center Plaza, Suite 300
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,367B
; FILING DATE: 07-06-95
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Villacorta, Gilberto M.
; REGISTRATION NUMBER: 34,038
; REFERENCE/DOCKET NUMBER: 2654-002A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 684-1111
; TELEFAX: (703) 684-1124
; TELEX:
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-480-367B-54

Query Match 85.7%; Score 18; DB 1; Length 4;
Best Local Similarity 75.0%; Pred. No. 3e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGDA 4
Db 1 RGDS 4

RESULT 14
US-08-487-221A-54
; Sequence 54, Application US/08487221A
; Patent No. 5593656
; GENERAL INFORMATION:
; APPLICANT: BELINKA JR, BENJAMIN A.
; APPLICANT: COUGHLIN, DANIEL J.
; APPLICANT: ALVAREZ, VERNON L.
; APPLICANT: WOOD, RICHARD
; TITLE OF INVENTION: METAL-BINDING TARGETED POLYPEPTIDE
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, McCLELLAND, MAIER &
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.

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; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,221A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/127,351
; FILING DATE: 28-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Villacorta, Gilberto M.
; REGISTRATION NUMBER: 34,038
; REFERENCE/DOCKET NUMBER: 4980-004-44
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248955 OPAT UR
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-487-221A-54

Query Match 85.7%; Score 18; DB 1; Length 4;
Best Local Similarity 75.0%; Pred. No. 3e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGDA 4
Db 1 RGDS 4

RESULT 15
US-08-480-370-54
; Sequence 54, Application US/08480370
; Patent No. 5609847
; GENERAL INFORMATION:
; APPLICANT: BELINKA JR, BENJAMIN A.
; APPLICANT: COUGHLIN, DANIEL J.
; APPLICANT: ALVAREZ, VERNON L.
; APPLICANT: WOOD, RICHARD
; TITLE OF INVENTION: METAL-BINDING TARGETED POLYPEPTIDE
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, McCLELLAND, MAIER &
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,370
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/127,351
; FILING DATE: 28-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Villacorta, Gilberto M.

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; REGISTRATION NUMBER: 34,038
; REFERENCE/DOCKET NUMBER: 4980-004-44
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-480-370-54

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Query Match      85.7%; Score 18; DB 1; Length 4;
Best Local Similarity 75.0%; Pred. No. 3e+05; 0; Indels 0; Gaps 0;
Matches 3; Conservative 1; Mismatches 0;

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QY 1 RGDA 4
Db 1 RGDS 4

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Search completed: February 26, 2004, 09:35:27
Job time : 24 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 26, 2004, 09:38:36 ; Search time 21 Seconds
(without alignments)

64.128 Million cell updates/sec

Title: US-09-909-348-4

Perfect score: 71

Sequence: 1 RGDACXGDSGGPXV 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 268

Minimum DB seq length: 14

Maximum DB seq length: 14

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 78:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	39.4	14	2 PH0800	T-cell receptor al
2	22	31.0	14	2 S17766	beta-glucosidase (
3	20	28.2	14	2 PH1321	IG heavy chain DJ
4	19	26.8	14	2 S23376	collagen alpha cha
5	19	26.8	14	2 PH0747	T-cell receptor be
6	17	23.9	14	2 S36852	ribosomal protein
7	17	23.9	14	2 S09721	2S albumin small c
8	17	23.9	14	2 PH0776	T-cell receptor al
9	17	23.9	14	2 PH0765	T-cell receptor be
10	17	23.9	14	2 PH0755	T-cell receptor be
11	16	22.5	14	2 B29743	translation initia
12	16	22.5	14	2 PH0232	IG heavy chain CRD
13	16	22.5	14	2 PH0232	IG heavy chain CRD
14	16	22.5	14	2 PH0254	IG heavy chain CRD
15	16	22.5	14	2 S47366	T-cell antigen rec
16	16	22.5	14	2 PC7075	guanylate cyclase
17	16	22.5	14	2 PH1598	IG H chain V-D-J r
18	16	22.5	14	2 PH1448	T-cell receptor al
19	16	22.5	14	2 PH0804	T-cell receptor al
20	16	22.5	14	2 PH1450	T-cell receptor al
21	16	22.5	14	2 PH0753	T-cell receptor be
22	15	21.1	14	2 B61309	lutropin beta chai
23	15	21.1	14	2 I39753	nitrogenase (EC 1
24	15	21.1	14	2 P30278	ribulose-bisphosph
25	15	21.1	14	2 PAC096	pyruvate decarboxy
26	15	21.1	14	2 PH1757	T cell receptor al
27	15	21.1	14	2 PH1766	T cell receptor al
28	15	21.1	14	2 S57574	T cell receptor V-
29	15	21.1	14	2 PH0792	T-cell receptor al

30	15	21.1	14	2 A17150	glucose 1-dehydrog
31	14	19.7	14	2 S59495	formate dehydrogen
32	14	19.7	14	2 S74128	superoxide dismuta
33	14	19.7	14	2 E33098	214K exoantigen (v
34	14	19.7	14	2 A39703	tubulin beta-3 cha
35	14	18.7	14	2 A43847	IG mu chain V regi
36	14	19.7	14	2 PH1628	IG H chain V-D-J r
37	14	19.7	14	2 PH1639	IG H chain V-D-J r
38	14	19.7	14	2 PH0762	T-cell receptor be
39	13	18.3	14	1 NTKN1M	alpha-conotoxin MI
40	13	18.3	14	2 A58963	alpha-conotoxin Ch
41	13	18.3	14	2 S27140	hypothetical prote
42	13	18.3	14	2 A32654	fibrinopeptide A -
43	13	18.3	14	2 B58502	36K kidney stone p
44	13	18.3	14	2 PAC109	porin por 1B - Ara
45	13	18.3	14	2 PAC045	porin por1 - Arabi

ALIGNMENTS

RESULT 1

PH0800

T-cell receptor alpha chain (J3) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C;Accession: PH0800

R;Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.

J. Exp. Med. 174, 1371-1383, 1991

A;Title: T cell receptor genes in a series of class I major histocompatibility complex-r allelic exclusion and antigen-specific repertoire.

A;Reference number: PH0746; MUID:92078846; PMID:1836010

A;Accession: PH0800

A;Molecule type: mRNA

A;Residues: 1-14 <CAS>

A;Cross-references: EMBL:X60907

A;Experimental source: T lymphocyte

C;Keywords: T-cell receptor

Query Match 39.4%; Score 28; DB 2; Length 14;
Best Local Similarity 57.1%; Pred. No. 1.8e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 CXGDSGG 11

DB 1 CAGNQQG 7

RESULT 2

S17766

beta-glucosidase (EC 3.2.1.21) A - almond (fragments)

C;Species: Prunus dulcis (almond)

C;Date: 22-Nov-1993 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997

C;Accession: S17766

R;Legler, G.; Harder, A.

Biochim. Biophys. Acta 524, 102-108, 1978

A;Title: Amino acid sequence at the active site of beta-glucosidase A from bitter almonds

A;Reference number: S17766; MUID:78187421; PMID:418615

A;Accession: S17766

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-14 <LEG>

C;Keywords: glycosidase; hydrolase

Query Match 31.0%; Score 22; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GDSGG 10

DB 8 GDSGG 11

```

RESULT 3
PHI321
IG heavy chain DJ region (clone C72-96R) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C:Accession: PHI321
R:Kasserman, R.; Galli, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A:Title: Predominance of fetal type DJH joining in young children with B precursor lymph
A:Reference number: PHI302; MUID:93094761; PMID:1460419
A:Accession: PHI321
A:Molecule type: DNA
A:Residues: 1-14 <WAS>
C:Keywords: heterotetramer; immunoglobulin

Query Match      28.2%; Score 20; DB 2; Length 14;
Best Local Similarity 42.9%; Pred. No. 3.7e+03;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 ACXGDSG 10
   :|||:|
Db 4 SCLGATG 10

RESULT 4
S23376
collagen alpha chain - polychaete (Alvinella pompejana) (fragment)
C:Species: Alvinella pompejana
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 29-May-1998
C:Accession: S23376
R:Gall, F.; Wiedemann, H.; Mann, K.; Kuehn, K.; Timpl, R.; Engel, J.
J. Mol. Biol. 221, 209-223, 1991
A:Title: Molecular characterization of cuticle and interstitial collagens from worms col
A:Reference number: S17581; MUID:192015209; PMID:1920405
A:Accession: S23376
A:Molecule type: protein
A:Residues: 1-14 <GAL>

Query Match      26.8%; Score 19; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GGP 12
   :|||
Db 5 GGP 7

RESULT 5
PHO747
T-cell receptor beta chain (M1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PHO747
R:Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A:Title: T cell receptor genes in a series of class I major histocompatibility complex-r
allelic exclusion and antigen-specific repertoire.
A:Reference number: PHO746; MUID:92078846; PMID:1836010
A:Accession: PHO747
A:Molecule type: mRNA
A:Residues: 1-14 <CAS>
A:Cross-references: EMBL:X60838
A:Experimental source: T lymphocyte
C:Keywords: T-cell receptor

Query Match      26.8%; Score 19; DB 2; Length 14;
Best Local Similarity 42.9%; Pred. No. 5.4e+03;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 CXGDSGG 11
   :|||
Db 1 CAWGTGG 7

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```

RESULT 6
S36892
ribosomal protein - Mycobacterium bovis (fragment)
C:Species: Mycobacterium bovis
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Jan-1995
C:Accession: S36892
R:Ohara, N.; Kimura, M.; Higashi, Y.; Yamada, T.
FEBS Lett. 331, 9-14, 1993
A:Title: Isolation and amino acid sequence of the 30S ribosomal protein S19 from Mycobac
A:Reference number: S36887; MUID:94009653; PMID:8405418
A:Accession: S36892
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-14 <OHA>

Query Match      23.9%; Score 17; DB 2; Length 14;
Best Local Similarity 33.3%; Pred. No. 1.1e+04;
Matches 4; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 3 DACKGDSGGPXV 14
   :|||
Db 2 EAKTGAKAPRV 13

RESULT 7
S09721
2S albumin small chain nIII - rape (fragments)
C:Species: Brassica napus (rape)
C>Date: 19-Mar-1997 #sequence_revision 13-Mar-1998 #text_change 13-Mar-1998
C:Accession: S09721
R:Monsalve, R.I.; Menendez-Arias, L.; Lopez-Otin, C.; Rodriguez, R.
FEBS Lett. 263, 209-212, 1990
A:Title: beta-turns as structural motifs for the proteolytic processing of seed proteins
A:Reference number: S09720; MUID:90242974; PMID:2185951
A:Accession: S09721
A:Molecule type: protein
A:Residues: 1-9;10-14 <MON>
A:Experimental source: seed

Query Match      23.9%; Score 17; DB 2; Length 14;
Best Local Similarity 75.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 SGGP 12
   :|||
Db 1 SAGP 4

RESULT 8
PHO776
T-cell receptor alpha chain (M1 V-alpha-8.P3.3) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PHO776
R:Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A:Title: T cell receptor genes in a series of class I major histocompatibility complex-r
allelic exclusion and antigen-specific repertoire.
A:Reference number: PHO746; MUID:92078846; PMID:1836010
A:Accession: PHO776
A:Molecule type: mRNA
A:Residues: 1-14 <CAS>
A:Cross-references: EMBL:X60873
A:Experimental source: T lymphocyte
C:Keywords: T-cell receptor

Query Match      23.9%; Score 17; DB 2; Length 14;
Best Local Similarity 42.9%; Pred. No. 1.1e+04;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 CXGDSGG 11
   :|||

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Db 1 CALGTGG 7

RESULT 9
PH0765
T-cell receptor beta chain (H1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Nov-1999
C:Accession: PH0765
R:Casanova, J.L.; Romero, P.; Widmann, C.; Kourileky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A:Title: T cell receptor genes in a series of class I major histocompatibility complex-
allelic exclusion and antigen-specific repertoire.
A:Reference number: PH0746; MUID:92078846; PMID:1836010
A:Accession: PH0765
A:Molecule type: mRNA
A:Residues: 1-14 <CAS>
A:Cross-references: EMBL:X60859; NID:G51139; PID:CAA43249.1; PID:G51140
A:Experimental source: T lymphocyte
C:Keywords: T-cell receptor

Query Match 23.9%; Score 17; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGD 3
|||
Db 7 RGD 9

RESULT 10
PH0755
T-cell receptor beta chain (QA11.3.2) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Nov-1999
C:Accession: PH0755
R:Casanova, J.L.; Romero, P.; Widmann, C.; Kourileky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A:Title: T cell receptor genes in a series of class I major histocompatibility complex-
allelic exclusion and antigen-specific repertoire.
A:Reference number: PH0746; MUID:92078846; PMID:1836010
A:Accession: PH0755
A:Molecule type: mRNA
A:Residues: 1-14 <CAS>
A:Cross-references: EMBL:X60849; NID:G53876; PID:CAA43240.1; PID:G53877
A:Experimental source: T lymphocyte
C:Keywords: T-cell receptor

Query Match 23.9%; Score 17; DB 2; Length 14;
Best Local Similarity 37.5%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5 CXGDSGGP 12
|||
Db 1 CASRPGQP 8

RESULT 11
B29743
translation initiation factor eIF-2 alpha chain-associated kinase phosphopeptide - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 31-Dec-1998 #sequence_revision 31-Dec-1998 #text_change 31-Oct-1997
C:Accession: B29743
R:Rose, D.W.; Wettenhall, R.E.H.; Kudlicki, W.; Kramer, G.; Hardesty, B.
Biochemistry 26, 6583-6587, 1987
A:Title: The 90-kilodalton peptide of the heme-regulated eIF-2-alpha kinase has sequence
similarity to the 90-kilodalton peptide of the heme-regulated eIF-2-alpha kinase
A:Reference number: A90521; MUID:88107571; PMID:3427028
A:Accession: B29743
A:Molecule type: protein
A:Residues: 1-14 <ROS>
A:Experimental source: reticulocyte
C:Superfamily: heat shock protein 90

Query Match 22.5%; Score 16; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.7e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 DSG 10
|||
Db 11 DSG 13

RESULT 12
PT0232
Ig heavy chain CRD3 region (clone 1-124) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0232
R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and j
A:Reference number: PT0222; MUID:91108337; PMID:1899102
A:Accession: PT0232
A:Molecule type: DNA
A:Residues: 1-14 <YAM>
A:Experimental source: B lymphocyte
C:Keywords: heterotetramer; immunoglobulin

Query Match 22.5%; Score 16; DB 2; Length 14;
Best Local Similarity 75.0%; Pred. No. 1.7e+04;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 DSGG 11
|||
Db 6 DSSG 9

RESULT 13
PT0252
Ig heavy chain CRD3 region (clone 2-109D) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0252
R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and j
A:Reference number: PT0222; MUID:91108337; PMID:1899102
A:Accession: PT0252
A:Molecule type: DNA
A:Residues: 1-14 <YAM>
A:Experimental source: B lymphocyte
C:Keywords: heterotetramer; immunoglobulin

Query Match 22.5%; Score 16; DB 2; Length 14;
Best Local Similarity 75.0%; Pred. No. 1.7e+04;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 DSGG 11
|||
Db 7 DSSG 10

RESULT 14
PT0254
Ig heavy chain CRD3 region (clone 2-115A) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0254
R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and j
A:Reference number: PT0222; MUID:91108337; PMID:1899102
A:Accession: PT0254
A:Molecule type: DNA
A:Residues: 1-14 <YAM>
A:Experimental source: B lymphocyte

C;Keywords: heterotetramer; immunoglobulin

Query Match 22.5%; Score 16; DB 2; Length 14;
Best Local Similarity 75.0%; Pred. No. 1.7e+04;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 DSGG 11
|||
Db 8 DSGG 11

RESULT 15

S47366
T-cell antigen receptor VJ junction beta chain - human
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C;Accession: S47366
R;Lehner, P.J.
submitted to the EMBL Data Library, August 1994
A;Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T c
A;Reference number: S47355
A;Accession: S47366
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-14 <LEH>
A;Cross-references: EMBL:235691; NID:G527473; PIDN:CAA84760.1; PID:G527474
C;Keywords: T-cell receptor

Query Match 22.5%; Score 16; DB 2; Length 14;
Best Local Similarity 57.1%; Pred. No. 1.7e+04;
Matches 4; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

QY 5 CXGDSGG 11
|||
Db 3 CAG--GG 7

Search completed: February 26, 2004, 09:41:38
Job time : 22 secs

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OM protein - protein search, using sw model

Run on: February 26, 2004, 09:35:31 ; Search time 11 seconds
(without alignments)

66.271 Million cell updates/sec

Title: US-09-909-348-4

Perfect score: 71

Sequence: 1 RGDACXGDSGGPXV 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 76

Minimum DB seq length: 14

Maximum DB seq length: 14

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	31.0	14	1	TAT_HV1W2
2	22	31.0	14	1	TAT_HV1Z8
3	16	22.5	14	1	KPPI_SELMI
4	15	21.1	14	1	SAP2_ARBP
5	14.5	20.4	14	1	RS19_CLOPP
6	14.5	20.4	14	1	RS19_LOEP
7	14	19.7	14	1	P1BA_HORSE
8	14	19.7	14	1	F1BB_MANLE
9	13	18.3	14	1	FXAI_CONCN
10	13	18.3	14	1	FXAI_CONNA
11	13	18.3	14	1	NET2_FASHE
12	13	18.3	14	1	PK66_PERAM
13	13	18.3	14	1	UN46_CLOPA
14	12	16.9	14	1	CAT2_FASHE
15	12	16.9	14	1	COCO_LIMPO
16	12	16.9	14	1	COCO_LIMPO
17	12	16.9	14	1	UN37_CLOPA
18	11	15.5	14	1	GLPK_STRGR
19	11	15.5	14	1	RS19_PRUP
20	11	15.5	14	1	SK3_LEICU
21	10	14.1	14	1	CXIA_CONBE
22	10	14.1	14	1	GLGS_SPIOL
23	10	14.1	14	1	GR75_CANFA
24	10	14.1	14	1	JAPI_RANJA
25	10	14.1	14	1	KARA_BROPL
26	10	14.1	14	1	MARI_ALTP
27	10	14.1	14	1	MY14_PHEVI
28	10	14.1	14	1	NSK2_SABU
29	10	14.1	14	1	PHI_PRUSE
30	10	14.1	14	1	RS19_PPWRP
31	10	14.1	14	1	SMS1_MYOSC
32	10	14.1	14	1	SMS1_ALIMI
33	10	14.1	14	1	SODN_STRGR

34 10 14.1 14 1 TKNM_RANVA
35 10 14.1 14 1 UC15_MAIZE
36 9 12.7 14 1 ADPA_TENNO
37 9 12.7 14 1 SGAT_MOUSE
38 9 12.7 14 1 CRBL_VESOR
39 9 12.7 14 1 HV14_PIG
40 9 12.7 14 1 IF2G_RAT
41 9 12.7 14 1 MAST_VESXA
42 9 12.7 14 1 MCR2_METTM
43 9 12.7 14 1 PSAG_CUCSA
44 9 12.7 14 1 UHAL_CANFA
45 8 11.3 14 1 UHAL_ALYOB

ALIGNMENTS

RESULT 1

TAT_HV1W2

ID TAT_HV1W2 STANDARD; PRT; 14 AA.

AC P12509;

DT 01-OCT-1989 (Rel. 12, Created)

DT 01-OCT-1989 (Rel. 12, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE TAT protein (Transactivating regulatory protein) (Fragment).

GN TAT.

OS Human immunodeficiency virus type 1 (WMJ2 isolate) (HIV-1).

OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.

OX NCBI_TaxID=11705;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=6235450; PubMed=3012778;

RA Hahn B.H., Shaw G.M., Taylor M.E., Redfield R.R., Markham P.D.,

Salauddin S.Z., Wong-Staal F., Gallo R.C., Parks E.S., Parks W.P.;

"Genetic variation in HIV-III/LAV over time in patients with AIDS or

at risk for AIDS."

RL Science 232:1548-1553 (1986).

CC -!- FUNCTION: Transcriptional regulator that acts by binding to the

trans-activating responsive sequence (TAR) RNA element and

activates transcription initiation and/or elongation from the LTR

promoter.

CC -!- SUBUNIT: Binds cyclin T1 (By similarity).

CC -!- SUBCELLULAR LOCATION: Nuclear; nucleolar.

CC -!- MISCELLANEOUS: ISOLATES WMJ1, WMJ2, AND WMJ3 WERE OBTAINED FROM

BLOOD SAMPLES SEQUENTIALLY TAKEN FROM A TWO-YEAR OLD HAITIAN WHO

WAS PERINATALLY INFECTED BY HER MOTHER.

CC -----

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CC -----

CC EMBL; M12507; AAB12991.1; -.

DR HIV; M12507; TATSWMJ2.

DR Transcription regulation; Activator; RNA-binding; Nuclear protein;

KW AIDS..

FT NON TER 1 1

FT SEQUENCE 14 AA; 1467 MW; 37CC737BEEF67AA8 CRC64;

CC

Query Match 31.0%; Score 22; DB 1; Length 14;

Best Local Similarity 66.7%; Pred. No. 5.4e-02;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 GDGGGP 12

DB 7 GDPTGP 12

RESULT 2

TAT_HV1Z8

ID TAT HV12S STANDARD; PRT; 14 AA.
AC P12511;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE TAR protein (Transactivating regulatory protein) (Fragment).
GN TAT.
OS Human immunodeficiency virus type 1 (Z-84 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11681;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88281278; PubMed=3395517;
RA Yourho J., Josephs S.F., Reitz M.S. Jr., Zagury D., Wong-Staal F.,
RA Gallo R.C.;
RT "Nucleotide sequence analysis of the env gene of a new Zairian
RT isolate of HIV-1.";
RL AIDS Res. Hum. Retroviruses 4:165-173(1988).
CC -!- FUNCTION: Transcriptional regulator that acts by binding to the
CC trans-activating responsive sequence (TAR) RNA element and
CC activates transcription initiation and/or elongation from the LTR
CC promoter.
CC -!- SUBUNIT: Binds cyclin T1 (By similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear; nucleolar.
CC -!- MISCELLANEOUS: THE Z-84 ISOLATE WAS TAKEN FROM A 54 YEAR-OLD
CC ZAIREAN MALE.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC
CC EMBL; J03653; AA444685.1; -.
CC HIV; J03653; TATSVY1.
CC Transcription regulation; Activator; RNA-binding; Nuclear protein;
CC AIDS.
CC NON TER 1
CC SEQUENCE 14 AA; 1453 MW; 37CC737BF82D7AA8 CRC64;

Query Match 31.0%; Score 22; DB 1; Length 14;
Best Local Similarity 66.7%; Pred. No. 5.4e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 GDSGGP 12
DB 7 GDTGTP 12

RESULT 3
ID KPPI SELMI STANDARD; PRT; 14 AA.
AC P25933;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Phosphoribulokinase, 40 kDa subunit (EC 2.7.1.19) (Phosphopentokinase)
DE (Fragment).
DE Selenastrum minutum.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Selenastraceae;
OC Selenastrum.
OX NCBI_TaxID=39955;
RN [1]
RP SEQUENCE.
RA Lin M., Turpin D.H.;
RT "Purification and molecular and immunological characterization of a
RT unique phosphoribulokinase from the green alga Selenastrum minutum.";
RL Plant Physiol. 98:82-88(1992).
CC -!- CATALYTIC ACTIVITY: ATP + D-ribulose 5-phosphate = ADP + D-
CC ribulose 1,5-bisphosphate.
CC -!- PATHWAY: Calvin cycle.

CC -!- SUBUNIT: Heterodimer of a 40 kDa and a 41 kDa subunit.
CC -!- SIMILARITY: Belongs to the phosphoribulokinase family.
CC InterPro; IPR006082; PRK.
DR PROSITE; PS00567; PHOSPHORIBULOKINASE; PARTIAL.
KW Transferase; Kinase; Calvin cycle; ATP-binding.
FT NON TER 14
SQ SEQUENCE 14 AA; 1379 MW; C481D8CD2F891062 CRC64;

Query Match 22.5%; Score 16; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 DSG 10
DB 12 DSG 14

RESULT 4
ID SAP2 ARBPU STANDARD; PRT; 14 AA.
AC P11760;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Resact (Sperm-activating peptide) (SAP-IIA).
OS Arbacia punctulata (Punctuate sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa; Arbacia.
OC Echinoidea; Euechinoidea; Echinacea; Arbacoidea; Arbacoidea; Arbacia.
OX NCBI_TaxID=7641;
RN [1]
RP SEQUENCE.
RC TISSUE=egg;
RX MEDLINE=85054981; PubMed=6150045;
RA Suzuki N., Shimomura H., Radany E.W., Ramarao C.S., Ward G.E.,
RA Bentley J.K., Garbers D.L.;
RT "A peptide associated with eggs causes a mobility shift in a major
RT plasma membrane protein of spermatozoa.";
RL J. Biol. Chem. 259:14874-14879(1984).
RN [2]
RP DISULFIDE BOND.
RX MEDLINE=92097763; PubMed=1756858;
RA Yoshino K.-I., Takao T., Shimonishi Y., Suzuki N.;
RT "Determination of the amino acid sequence of an intramolecular
RT disulfide linkage-containing sperm-activating peptide by tandem mass
RT spectrometry.";
RL FEBS Lett. 294:179-182(1991).
CC -!- FUNCTION: Cause stimulation of sperm respiration and motility
CC through intracellular alkalization, transient elevations of
CC cAMP, cGMP and calcium levels in sperm cells, and transient
CC activation and subsequent inactivation of the membrane form of
CC guanylate cyclase.
CC -!- SIMILARITY: SMALL TO S.PURPURATUS SPERACT.
KW Amidation.
FT DISULFID 1 8
FT MOD RES 14 14
SQ SEQUENCE 14 AA; 1246 MW; 39745AA33EBE41B8 CRC64;

Query Match 21.1%; Score 15; DB 1; Length 14;
Best Local Similarity 57.1%; Pred. No. 7.7e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

QY 5 CXGDSGG 11
DB 8 CVG-GG 12

RESULT 5
ID RS19 CLOPP STANDARD; PRT; 14 AA.
AC Q46228;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DT

DE 30S ribosomal protein S19 (Fragment).
GN RPS19 OR RPS19
OS Clover proliferation phytoplasma.
OC Bacteria; Firmicutes; Mollicutes; Acholoplasmatales;
OC Acholoplasmataceae; Phytoplasma.
OX NCBI_TaxID=35776;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94350802; PubMed=8071198;
RA Gundersen D.E., Lee I.M., Rehner S.A., Davis R.E., Kingsbury D.T.;
RT "Phylogeny of mycoplasma-like organisms (phytoplasmas): a basis for
their classification."
RL J. Bacteriol. 176:5244-5254(1994).
CC -!- FUNCTION: Protein S19 forms a complex with S13 that binds strongly
to the 16S ribosomal RNA (By similarity).
CC -!- SIMILARITY: Belongs to the S19p family of ribosomal proteins.
CC
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CC
CC EMBL; L27011; AAA83936.1; -.
DR HAMAP; MF 00531; -; 1.
DR InterPro; IPR002222; Ribosomal_S19.
DR PROSITE; PS00323; RIBOSOMAL_S19; PARTIAL.
KW Ribosomal protein; rRNA-binding.
FT NON_TER 1
SQ SEQUENCE 14 AA; 1642 MW; 20C478EB9FFFE4A8 CRC64;
Query Match 20.4%; Score 14.5; DB 1; Length 14;
Best Local Similarity 62.5%; Pred. No. 9.2e+03;
Matches 5; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
OY 1 RGDACXGD 8
DB 2 RGHK-KGD 8
RESULT 6
RS19 LOWER STANDARD; PRT; 14 AA.
AC Q48878; 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 30S ribosomal protein S19 (Fragment).
GN Loofah witches'-broom phytoplasma.
OC Bacteria; Firmicutes; Mollicutes; Acholoplasmatales;
OC Acholoplasmataceae; Phytoplasma.
OX NCBI_TaxID=35773;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94350802; PubMed=8071198;
RA Gundersen D.E., Lee I.M., Rehner S.A., Davis R.E., Kingsbury D.T.;
RT "Phylogeny of mycoplasma-like organisms (phytoplasmas): a basis for
their classification."
RL J. Bacteriol. 176:5244-5254(1994).
CC -!- FUNCTION: Protein S19 forms a complex with S13 that binds strongly
to the 16S ribosomal RNA (By similarity).
CC -!- SIMILARITY: Belongs to the S19p family of ribosomal proteins.
CC
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CC

CC EMBL; L27027; AAA83944.1; -.
DR HAMAP; MF 00531; -; 1.
DR InterPro; IPR002222; Ribosomal_S19.
DR PROSITE; PS00323; RIBOSOMAL_S19; PARTIAL.
KW Ribosomal protein; rRNA-binding.
FT NON_TER 1
SQ SEQUENCE 14 AA; 1642 MW; 20C478EB9FFFE4A8 CRC64;
Query Match 20.4%; Score 14.5; DB 1; Length 14;
Best Local Similarity 62.5%; Pred. No. 9.2e+03;
Matches 5; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
OY 1 RGDACXGD 8
DB 2 RGHK-KGD 8
RESULT 7
FIBB HORSE STANDARD; PRT; 14 AA.
AC P14452;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN FGA.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE.
RA Blomback B., Blomback M., Grondahl N.J.;
RT "Studies on fibrinopeptides from mammals."
RL Acta Chem. Scand. 19:1789-1791(1965).
CC -!- FUNCTION: Fibrinogen has a double function: yielding monomers that
polymerize into fibrin and acting as a cofactor in platelet
aggregation.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
(ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
which cleaves fibrinopeptides A and B from alpha and beta chains,
and thus exposes the N-terminal polymerization sites responsible
for the formation of the soft clot.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 14 FIBRINOPEPTIDE A.
FT NON_TER 14
SQ SEQUENCE 14 AA; 1517 MW; 4E998EB63C2A15E7 CRC64;
Query Match 19.7%; Score 14; DB 1; Length 14;
Best Local Similarity 50.0%; Pred. No. 1.1e+04;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
OY 8 DSGG 11
DB 9 EGGG 12
RESULT 8
FIBB MANLE STANDARD; PRT; 14 AA.
AC P14474;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN FGB.
OS Mandrillus leucophaeus (Drill) (Papio leucophaeus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoinae; Mandrillus.
OX NCBI_TaxID=9568;

OS Fasciola hepatica (liver fluke).
 OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
 OC Echinostomida; Echinostomata; Fasciolidae; Fasciolidae; Fasciola.
 OX NCBI_TaxID=6192;
 RN [1]
 RP SEQUENCE.
 RA MEDLINE=95366993; PubMed=7639732;
 RX Tkalec J., Ashman K., Meusen E.,
 RT "Fasciola hepatica: rapid identification of newly excysted juvenile
 proteins";
 RL Biochem. Biophys. Res. Commun. 213:169-174(1995).
 CC -!- DEVELOPMENTAL STAGE: Expressed at the newly excysted juvenile
 CC STAGE.
 FT NON TER 14 14
 SQ SEQUENCE 14 AA; 1581 MW; 9E0F0090CC8C0DF1 CRC64;
 Query Match 18.3%; Score 13; DB 1; Length 14;
 Best Local Similarity 66.7%; Pred. No. 1.6e+04;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 8 DSG 10
 DB 3 DNG 5
 RESULT 12
 PK6_PERAM STANDARD; PRT; 14 AA.
 AC P82693;
 DT 16-OCT-2001 (Rel. 40, Created).
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE Pyrokinin-6 (Pea-PK-6) (EXPRIL-amide).
 OS Piriplaneta americana (American cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
 OC Blattidae; Periplaneta.
 OX NCBI_TaxID=6978;
 RN [1]
 RP SEQUENCE, FUNCTION, TISSUE SPECIFICITY, AND MASS SPECTROMETRY.
 RC TISSUE=Abdominal perisymphathetic organs, and Corpora cardiaca;
 RX MEDLINE=20189894; PubMed=10723010;
 RA Predel R., Eckert M.;
 RT "Tagma-specific distribution of FXPRILamides in the nervous system of
 the American cockroach";
 RL J. Comp. Neurol. 419:352-363(2000).
 CC -!- FUNCTION: Shows a weakly myoactive action.
 CC -!- TISSUE SPECIFICITY: Corpora alata and to a lesser extent in
 abdominal perisymphathetic organs.
 CC -!- MASS SPECTROMETRY: MW=1590.8; METHOD=VALDI.
 CC -!- SIMILARITY: Belongs to the pyrokinin family.
 DR InterPro; IPR001484; Pyrokinin.
 DR PROSITE; PS00539; PYROKININ.
 KW Amidation; Pyrokinin.
 FT MOD_RES 14 14
 SQ SEQUENCE 14 AA; 1592 MW; 3966CC3FF384A998 CRC64;
 Query Match 18.3%; Score 13; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.6e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 11 GP 12
 DB 11 GP 12
 RESULT 13
 UN46_CLOPA STANDARD; PRT; 14 AA.
 AC P81362;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)

DE Unknown protein CP 46 from 2D-page (Fragment).
 OS Clostridium pasteurianum.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=1501;
 RN [1]
 RP SEQUENCE.
 RA STRAIN=W5;
 RX MEDLINE=98291870; PubMed=9629918;
 RT Flengsrud R., Skjeldal L.;
 RT "Two-dimensional gel electrophoresis separation and N-terminal
 sequence analysis of proteins from Clostridium pasteurianum W5";
 RL Electrophoresis 19:802-806(1998).
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 5.4, ITS MW IS: 38.2 kDa.
 FT NON TER 14 14
 SQ SEQUENCE 14 AA; 1550 MW; 198078F4C0367170 CRC64;
 Query Match 18.3%; Score 13; DB 1; Length 14;
 Best Local Similarity 42.9%; Pred. No. 1.6e+04;
 Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 2 GDACXGD 8
 DB 8 GNNIGD 14
 RESULT 14
 CAT2_FASHE STANDARD; PRT; 14 AA.
 ID P80342;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cathepsin L2 (EC 3.4.22.15) (Fragment).
 OS Fasciola hepatica (liver fluke).
 OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
 OC Echinostomida; Echinostomata; Fasciolidae; Fasciola.
 OX NCBI_TaxID=6192;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=94307282; PubMed=8033913;
 RA Dowd A.J., Smith A.M., McGonigle S., Dalton J.P.;
 RT "Purification and characterisation of a second cathepsin L proteinase
 secreted by the parasitic trematode Fasciola hepatica";
 RL Eur. J. Biochem. 223:91-98(1994).
 CC -!- FUNCTION: Thiol protease that assists the parasite in burrowing
 through the gut wall and liver of its mammalian host.
 CC -!- CATALYTIC ACTIVITY: Specificity close to that of papain. As
 compared to cathepsin B, cathepsin L exhibits higher activity
 towards protein substrates, but has little activity on Z-Arg-Arg-
 NHMe, and no peptidyl-dipeptidase activity.
 CC -!- SUBUNIT: Dimer of a heavy and a light chain linked by disulfide
 bonds.
 CC -!- SUBCELLULAR LOCATION: Lysosomal.
 CC -!- SIMILARITY: Belongs to peptidase family C1.
 DR MEROPS; C01.033;
 DR InterPro; IPR000169; SHPOT acsite.
 DR PROSITE; PS00139; THIOL_PROTEASE_CYS; PARTIAL.
 DR PROSITE; PS00639; THIOL_PROTEASE_HIS; PARTIAL.
 DR PROSITE; PS00640; THIOL_PROTEASE_ASN; PARTIAL.
 KW Hydrolase; Thiol protease; Lysosome.
 FT NON TER 14 14
 SQ SEQUENCE 14 AA; 1605 MW; 9CAEAB74E9DA110A CRC64;
 Query Match 16.9%; Score 12; DB 1; Length 14;
 Best Local Similarity 66.7%; Pred. No. 2.3e+04;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 8 DSG 10
 DB 10 ESG 12

```

RESULT 15
COCO LIMPO
ID _COCO_LIMPO STANDARD; PRT; 14 AA.
AC F3586;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cocoonase (EC 3.4.21.-) (Fragment).
OS Limulus polyphemus (Atlantic horseshoe crab).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
OC Limulidae; Limulus.
CX NCBI_taxid=6850;
RN [1]
RP SEQUENCE.
RX MEDLINE=78037243; PubMed=335821;
RA Law J.H., Dunn P.E., Kramer K.J.;
RT "Insect proteases and peptidases";
RL Adv. Enzymol. Relat. Areas Mol. Biol. 45:389-425(1977).
CC -!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-, Lys-.
CC -!- SUBCELLULAR LOCATION: Extracellular.
CC -!- SIMILARITY: Belongs to peptidase family S1.
DR MEROPS; S01.112; -.
DR InterPro; IPR001254; Peptidase S1.
DR PROSITE; PS00240; TRYPSIN_DOM; PARTIAL.
DR PROSITE; PS00134; TRYPSIN_HIS; PARTIAL.
DR PROSITE; PS00135; TRYPSIN_SER; PARTIAL.
KW Hydrolase; Serine protease.
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1452 MW; 1615PB1D73747570 CRC64;

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Query Match 16.9%; Score 12; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 10 GG 11
Db 3 GG 4

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Search completed: February 26, 2004, 09:41:05
Job time : 13 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 26, 2004, 09:38:57 ; Search time 39 Seconds

(without alignments)
113.263 Million cell updates/sec

Title: US-09-909-348-4

Perfect score: 71

Sequence: 1 RGDACXGDSGGPXV 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 420

Minimum DB seq length: 14

Maximum DB seq length: 14

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_25.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rviro.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	26	36.6	14	15 Q88400	Q88400 simian t-ly
2	22	31.0	14	15 Q8JDM3	Q8JDM3 human immun
3	22	31.0	14	15 Q8JDM7	Q8JDM7 human immun
4	22	31.0	14	15 Q8JDM0	Q8JDM0 human immun
5	21	29.6	14	10 Q9S939	Q9S939 beta vulgar
6	19	26.8	14	5 O18502	O18502 schistosoma
7	19	26.8	14	10 P82322	P82322 pisum sativ
8	19	26.8	14	10 Q7X950	Q7X950 malus domes
9	18	25.4	14	4 Q7Z7E2	Q7Z7E2 homo sapien
10	18	25.4	14	6 Q9TR83	Q9TR83 sus scrofa
11	17	23.9	14	3 Q8JUG5	Q8JUG5 ashbya goss
12	17	23.9	14	4 Q16045	Q16045 homo sapien
13	17	23.9	14	5 Q26075	Q26075 psammechinu
14	17	23.9	14	11 Q8CJA8	Q8CJA8 mus_musculu
15	16	22.5	14	2 Q8VQ14	Q8VQ14 micrococcu
16	16	22.5	14	4 Q8NIA6	Q8NIA6 homo sapien

17	16	22.5	14	13	Q9DE34
18	15	21.1	14	2	P96350
19	15	21.1	14	2	Q43905
20	15	21.1	14	4	Q81VK4
21	14	19.7	14	2	Q9R5M2
22	14	19.7	14	2	Q56750
23	14	19.7	14	2	Q46291
24	14	19.7	14	4	Q9NY40
25	14	19.7	14	4	Q9P0W1
26	14	19.7	14	10	Q9XGM4
27	14	19.7	14	10	P82340
28	14	19.7	14	12	O85578
29	13	18.3	14	2	Q9R5P6
30	13	18.3	14	2	Q54394
31	13	18.3	14	2	Q54081
32	13	18.3	14	7	Q8MH06
33	13	18.3	14	7	Q8MH35
34	13	18.3	14	7	Q8MH39
35	13	18.3	14	7	Q8MH18
36	13	18.3	14	7	Q8MH55
37	13	18.3	14	7	Q8MH40
38	13	18.3	14	7	Q8MH07
39	13	18.3	14	7	Q8MH04
40	13	18.3	14	7	Q8MH52
41	13	18.3	14	7	Q8MH26
42	13	18.3	14	7	Q8MH53
43	13	18.3	14	7	Q8MH20
44	13	18.3	14	7	Q8MH27
45	13	18.3	14	7	Q8MH05

ALIGNMENTS

RESULT 1

Q88400 PRELIMINARY; PRT; 14 AA.
AC Q88400;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Tax protein (Fragment).
GN TAX.
OS Simian T-lymphotropic virus 1.
OC Viruses; Retroid viruses; Retroviridae; Deltaretrovirus.
OX NCBI_TaxID=33747;
RN [1]
RP SEQUENCE FROM N.A.
EX MEDLINE=94082462; PubMed=8259665;
RA Sakana N.K., Herve V., Durand J.P., LeGuanno B., Diop O.M.,
RA Digoutte J.P., Mathiot C., Muller M.C., Love J.L., Benz P.M.,
RA Erensoy S., Barre-Sinoussi F., Poiesz B.J.;
RT "Seroepidemiologic, molecular, and phylogenetic analyses of simian T-
cell leukemia viruses (STLV-I) from various naturally infected monkey
species from central and western Africa.";
RL Virology 198;297-310(1993).
DR EMBL; L20363; AAA47870.1; .
DR GO; GO:0016563; F:transcriptional activator activity; IEA.
DR GO; GO:0045941; P:positive regulation of transcription; IEA.
DR InterPro; IPR004120; Tax.
DR Pfam; PF02959; Tax; 1.
FT NON TER 1 1
FT NON TER 14 14
SQ SEQUENCE 14 AA; 1394 MW; 8BA7726C9C6D387A CRC64;

Query Match 36.6%; Score 26; DB 15; Length 14;
Best Local Similarity 50.0%; Pred. No. 8.7e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 4; Gaps 1;

QY 2 GDCXGDP---SGG 11

Db 1 GDCVQGDWCPISSG 14

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RESULT 2
Q8JDM3 PRELIMINARY; PRT; 14 AA.
AC Q8JDM3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Truncated tat protein (Fragment).
GN TAT.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RX MEDLINE=22032414; PubMed=12036486;
RA Long E.M., Rainwater S.M., Lavreys L., Mandaliya K., Overbaugh J.;
RT "HIV Type 1 Variants Transmitted to Women in Kenya Require the CCR5
RT Coreceptor for Entry, Regardless of the Genetic Complexity of the
RT Infecting Virus.";
RL AIDS Res. Hum. Retroviruses 18:567-576(2002).
DR EMBL; AF407149; AAM66202.1; -.
FT NON TER 1
SQ SEQUENCE 14 AA; 1442 MW; 37C58F7BF82D7AA8 CRC64;

Query Match 31.0%; Score 22; DB 15; Length 14;
Best Local Similarity 66.7%; Pred. No. 4.le+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 GDSGGP 12
Db 7 GDPTGP 12

RESULT 3
Q8JDM7 PRELIMINARY; PRT; 14 AA.
AC Q8JDM7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Truncated tat protein (Fragment).
GN TAT.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RX MEDLINE=22032414; PubMed=12036486;
RA Long E.M., Rainwater S.M., Lavreys L., Mandaliya K., Overbaugh J.;
RT "HIV Type 1 Variants Transmitted to Women in Kenya Require the CCR5
RT Coreceptor for Entry, Regardless of the Genetic Complexity of the
RT Infecting Virus.";
RL AIDS Res. Hum. Retroviruses 18:567-576(2002).
DR EMBL; AF407148; AAM66198.1; -.
FT NON TER 1
SQ SEQUENCE 14 AA; 1442 MW; 37C58F7BF82D7AA8 CRC64;

Query Match 31.0%; Score 22; DB 15; Length 14;
Best Local Similarity 66.7%; Pred. No. 4.le+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 GDSGGP 12
Db 7 GDPTGP 12

RESULT 4
Q8JDM0 PRELIMINARY; PRT; 14 AA.
AC Q8JDM0;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

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DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Truncated tat protein (Fragment).
GN TAT.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RX MEDLINE=22032414; PubMed=12036486;
RA Long E.M., Rainwater S.M., Lavreys L., Mandaliya K., Overbaugh J.;
RT "HIV Type 1 Variants Transmitted to Women in Kenya Require the CCR5
RT Coreceptor for Entry, Regardless of the Genetic Complexity of the
RT Infecting Virus.";
RL AIDS Res. Hum. Retroviruses 18:567-576(2002).
DR EMBL; AF407150; AAM66205.1; -.
FT NON TER 1
SQ SEQUENCE 14 AA; 1442 MW; 37C58F7BF82D7AA8 CRC64;

Query Match 31.0%; Score 22; DB 15; Length 14;
Best Local Similarity 66.7%; Pred. No. 4.le+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 GDSGGP 12
Db 7 GDPTGP 12

RESULT 5
Q9S939 PRELIMINARY; PRT; 14 AA.
AC Q9S939;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE H(+)-translocating (Pyrophosphate-ENERGIZED) inorganic pyrophosphatase
DE beta-2 polypeptide (EC 3.6.1.1) (Fragment).
OS Beta vulgaris (Sugar beet).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Amaranthaceae; Beta.
OX NCBI_TaxID=161934;
RN [1]
RX MEDLINE=92179265; PubMed=1311852;
RA Sarafian V., Kim Y., Poole R.J., Rea P.A.;
RT "Molecular cloning and sequence of cDNA encoding the pyrophosphate-
RT energized vacuolar membrane proton pump of Arabidopsis thaliana.";
RL Proc Natl. Acad. Sci. U.S.A. 89:1775-1779(1992).
DR PIR; B38230; B38230.
DR GO; GO:0004427; F:inorganic diphosphatase activity; IEA.
SQ SEQUENCE 14 AA; 1250 MW; 23250CDB1EE0F048 CRC64;

Query Match 29.6%; Score 21; DB 10; Length 14;
Best Local Similarity 55.6%; Pred. No. 6e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 2; Gaps 1;

QY 3 DACXGDSGG 11
Db 1 DAC--DAAG 7

RESULT 6
O18502 PRELIMINARY; PRT; 14 AA.
AC O18502;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Lysophospholipase homolog (Fragment).
GN SMLPLH.
OS Schistosoma mansoni (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OC Schistosomatoidae; Schistosomatidae; Schistosoma.

```

OX NCBI_TaxID=6183;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Egyptian;
 RA Hamdan F.F., Ribeiro P.;
 RT "Cloning and sequence analysis of a lysophospholipase homologue from
 RT Schistosoma mansoni.";
 RL Parasitol. Res. 84:839-842 (1998).
 DR EMBL: AF066679; AAC62255.1; -;
 FT NON TER 14 14
 SQ SEQUENCE 14 AA; 1541 MW; 48B847C2E5D89177 CRC64;

Query Match 26.8%; Score 19; DB 5; Length 14;
 Best Local Similarity 75.0%; Pred. No. 1.3e+04;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 GDSG 10
 |||
 Db 8 GDTG 11

RESULT 7
 P82322
 ID P82322 PRELIMINARY; PRT; 14 AA.
 AC P82322;
 DT 01-JUN-2000 (TrEMBLrel. 14, Created)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Unknown protein from 2D-page of thylakoid lumen (SPOT103) (Fragment).
 OS Pisum sativum (Garden pea).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids 1; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.
 OX NCBI_TaxID=3888;
 RN [1]
 RP SEQUENCE, SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.
 RC STRAIN=cv. DE GRACE; TISSUE=LEAF;
 RX MEDLINE=9011728; PubMed=10715320;
 RA Peltier J.-B., Friso G., Kalume D.E., Roepstorff P., Nilsson F.,
 RA Adamska I., van Wijk K.J.;
 RT "Proteomics of the chloroplast: systematic identification and
 RT targeting analysis of luminal and peripheral thylakoid proteins.";
 RL Plant Cell 12:319-341 (2000).
 CC -!- SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE LUMEN.
 CC -!- DEVELOPMENTAL STAGE: UNFOLDED AND FULLY DEVELOPED LEAVES.
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 5.7, IYS MW IS: 14.3 KDA.
 CC -!- SIMILARITY: TO A. THALIANA TL3E15.7.
 DR GO; GO:0009507; C:chloroplast; IEA.
 DR GO; GO:0009579; C:thylakoid; IEA.
 KW Chloroplast; Thylakoid.
 FT NON TER 14 14
 SQ SEQUENCE 14 AA; 1381 MW; 0023DD7E0B97066B CRC64;

Query Match 26.8%; Score 19; DB 10; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GGP 12
 |||
 Db 4 GGP 6

RESULT 8
 Q7X9S0
 ID Q7X9S0 PRELIMINARY; PRT; 14 AA.
 AC Q7X9S0;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Metallothionein-like protein (fragment).
 OS Malus domestica (Apple) (Malus sylvestris).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids 1; Rosales; Rosaceae; Maloideae; Malus.
 OX NCBI_TaxID=3750;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Granny Smith; TISSUE=Fruit flesh;
 RA Pathak N., Asif M., Solomos T.;
 RT "1-MCP induced transcripts in Granny Smith Apples stored at 1 C.";
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY277667; AAP34401.1; -;
 FT NON TER 1 1
 SQ SEQUENCE 14 AA; 1503 MW; 85ED164D6EB3E9A1 CRC64;

Query Match 26.8%; Score 19; DB 10; Length 14;
 Best Local Similarity 75.0%; Pred. No. 1.3e+04;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GDAC 5
 |||
 Db 3 GDNC 6

RESULT 9
 Q7Z7E2
 ID Q7Z7E2 PRELIMINARY; PRT; 14 AA.
 AC Q7Z7E2;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE A disintegrin and metalloprotease 33 (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Powell R.M., Wicks J., Holloway J.W., Holgate S.T., Davies D.D.;
 RT "Identification of novel ADAM33 transcripts that lack the
 RT metalloprotease domain.";
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY223853; AAP15442.1; -;
 KW Integrin; Metalloprotease; Protease.
 FT NON TER 14 14
 SQ SEQUENCE 14 AA; 1476 MW; 2B89AEBAD7DF207 CRC64;

Query Match 25.4%; Score 18; DB 4; Length 14;
 Best Local Similarity 60.0%; Pred. No. 1.9e+04;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CXGDS 9
 |||
 Db 10 CTGTS 14

RESULT 10
 Q9TR83
 ID Q9TR83 PRELIMINARY; PRT; 14 AA.
 AC Q9TR83;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE TRIKINASE (EC 2.7.1.28) (Fragment).
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=95132498; PubMed=7831203;
 RA Miwa I., Kito Y., Okuda J.;
 RL Prep. Biochem. 24:203-223 (1994).
 SQ SEQUENCE 14 AA; 1441 MW; C1F10CB1590001DD CRC64;

Query Match 25.4%; Score 18; DB 6; Length 14;
Best Local Similarity 75.0%; Pred. No. 1.9e+04;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 DSGG 11
DB 3 DSGG 6

RESULT 11
Q8UJG5 PRELIMINARY; PRT; 14 AA.
AC Q8UJG5;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE YLR191 (Fragment).
GN YLR191.
OS Ashbya gossypii (Yeast) (Eremothecium gossypii).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Ashbya.
OX NCBI_TaxID=33169;
RN [1]
RP SEQUENCE FROM N.A.
RA Alberti-Segui C., Dietrich F., Philippsen P.;
RT "Identification of kinesin-related proteins in the filamentous fungus
RT Ashbya gossypii.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DDJF databases.
DR EMBL; AF378569; AA087136.1; -;
FT NON_TER 1
SQ SEQUENCE 14 AA; 1205 MW; 36967F5A00467868 CRC64;

Query Match 23.9%; Score 17; DB 3; Length 14;
Best Local Similarity 50.0%; Pred. No. 2.8e+04;
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7 GDSGGP 12
DB 3 GSGTGP 8

RESULT 12
Q16045 PRELIMINARY; PRT; 14 AA.
AC Q16045;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE D3 dopamine receptor (Fragment).
GN D3R.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=93326145; PubMed=7916609;
RA Nagai Y., Ueno S., Saeki Y., Soga F., Yanagihara T.;
RT "Expression of the D3 dopamine receptor gene and a novel variant
RT transcript generated by alternative splicing in human peripheral blood
RT lymphocytes.";
RL Biochem. Biophys. Res. Commun. 194:368-374 (1993).
DR EMBL; S63845; AAB27543.2; -;
DR GO; GO:0004872; F:receptor activity; IEA.
FT NON_TER 1
SQ SEQUENCE 14 AA; 1586 MW; EA310BEF94CF1B1 CRC64;

Query Match 23.9%; Score 17; DB 4; Length 14;
Best Local Similarity 60.0%; Pred. No. 2.8e+04;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RGDAC 5
DB 4 RGPHC 8

RESULT 13
Q26075 PRELIMINARY; PRT; 14 AA.
AC Q26075;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Histone H2A (Fragment).
OS Psammecinus miliaris (Sand sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinoidea; Echinacea; Echinoida; Echinidae;
OC Psammecinus.
OX NCBI_TaxID=7660;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85140235; PubMed=2858095;
RA Nordstrom J.L., Hall S.L., Kessler M.M.;
RT "Polyadenylation of sea urchin histone RNA sequences in transfected
RT COS cells.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:1094-1098 (1985).
DR EMBL; M12542; AAA30028.1; -;
FT NON_TER 1
SQ SEQUENCE 14 AA; 1620 MW; 298A3F878A462268 CRC64;

Query Match 23.9%; Score 17; DB 5; Length 14;
Best Local Similarity 50.0%; Pred. No. 2.8e+04;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 SGGPXV 14
DB 6 SGPPNI 11

RESULT 14
Q8CJA8 PRELIMINARY; PRT; 14 AA.
AC Q8CJA8;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Methylenetetrahydrofolate reductase short isoform (Fragment).
GN MTHFR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SV;
RX MEDLINE=2257759; PubMed=12370778;
RA Tran P., Leclerc D., Chan M., Pai A., Hiou-Tim F., Wu Q., Goyette P.,
RA Artigas C., Milos R., Rozen R.;
RT "Multiple transcription start sites and alternative splicing in the
RT methylenetetrahydrofolate reductase gene result in two enzyme
RT isoforms.";
RL Mamm. Genome 13:483-492 (2002).
DR EMBL; AF404271; AAN40873.1; -;
DR MGD; MGI:106639; Mchfx.
FT NON_TER 14
SQ SEQUENCE 14 AA; 1472 MW; 28DD341AC1695CB8 CRC64;

Query Match 23.9%; Score 17; DB 11; Length 14;
Best Local Similarity 75.0%; Pred. No. 2.8e+04;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 SGGP 12

Db 8 SGSP 11

RESULT 15

QSVQ14 PRELIMINARY; PRT; 14 AA.
AC QSVQ14; 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE ERMWL leader peptide.
OS Micrococcus luteus (Micrococcus lysodeikticus).
OG Plasmid pMEC2.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Micrococccineae; Micrococcaceae; Micrococcus.
CX NCBI_taxID=1270;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MAW843;
RA Liebl W., Kloos W.E., Ludwig W.;
RT "Plasmid-borne macrolide-lincosamide-streptogramin B (MLS) resistance
in Micrococcus luteus.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF462611; AAL68826.1; -.
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
KW Plasmid.
SQ SEQUENCE 14 AA; 1625 MW; C6BF8E3F5CD58BCD CRC64;

Query Match 22.5%; Score 16; DB 2; Length 14;
Best Local Similarity 40.0%; Pred. No. 4.1e+04;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 10 GGPXV 14
Db 2 GSPSI 6

Search completed: February 26, 2004, 09:42:31
Job time : 42 secs

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OM protein - protein search, using sw model

Run on: February 26, 2004, 09:34:56 ; Search time 52 Seconds

(without alignments)
76,070 Million cell updates/sec

Title: US-09-909-348-4

Perfect score: 71
Sequence: 1 RGDAKXGDSGPXV 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 17938

Minimum DB seq length: 14
Maximum DB seq length: 14

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	67	94.4	14	5	Aau78375 Thrombin
2	67	94.4	14	5	Aae20158 Human thr
3	67	94.4	14	7	Abb80264 Thrombin
4	53	74.6	14	5	Aae17240 Human tra
5	53	74.6	14	5	Aae18999 Human mat
6	48	67.6	14	5	Aau80522 Epithelin
7	38	53.5	14	4	Aag73193 Protease
8	32	45.1	14	3	Aay53773 Linker of
9	32	45.1	14	4	Aae08818 Synthetic
10	32	45.1	14	5	Aae29569 Metallope
11	32	45.1	14	5	Aae29631 Metallope
12	30	42.3	14	2	Aar93584 Dopamine
13	30	42.3	14	2	Aaw10751 Thrombin
14	30	42.3	14	4	Abb56804 Human SNP
15	30	42.3	14	4	Abb56805 Human SNP
16	29	40.8	14	2	Aar69303 Gp IIB/II
17	29	40.8	14	2	Aaw50586 GPIIb/III
18	29	40.8	14	2	Aae25483 Tc-99m la
19	29	40.8	14	3	Aay54969 Peptide 1
20	29	40.8	14	3	Aay95454 GPIIb/III
21	29	40.8	14	4	Aag73186 Protease
22	29	40.8	14	4	Aag73194 Protease
23	27	38.0	14	2	Aaw69149 Neuronal
24	27	38.0	14	4	Aam00734 Human pro
25	27	38.0	14	5	Abp47204 Human Bly

ALIGNMENTS

RESULT 1
AAU78375
ID AAU78375 standard; peptide; 14 AA.

AC AAU78375;

XX 18-JUN-2002 (first entry)

XX Thrombin peptide derivative #2.

XX Thrombin; osteopathic; receptor; agonist; bone growth stimulation;
XX osteoinduction; farm animal; companion animal; laboratory animal;
XX bone graft; segmental bone gap; bone void; non-union fracture.

OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 7 /label= Glu, Gln

FT Misc-difference 13 /label= Phe, Met, Leu, His, Val

XX WO200205836-A2.

XX 24-JAN-2002.

XX 18-JUL-2001; 2001WO-US022641.

XX 19-JUL-2000; 2000US-0219300P.

XX (TEXA) UNIV TEXAS SYSTEM.

XX Carney DH, Crowther RS, Simmons DJ, Yang J, Redin WR;

XX WPI; 2002-303796/34.

XX Stimulating bone growth at a site in a subject in need of osteoinduction,
XX such as a site of bone graft, segmental bone gap, bone void or non-union
XX structure, by administering agonist of activated thrombin receptor.

XX Claim 10; Page 22; 27pp; English.

XX The invention describes a method of stimulating bone growth at a site in
XX a subject in need of osteoinduction. The method involves administering an
XX agonist to stimulate bone growth at a site in a subject (e.g. a farm
XX animal, companion animal or laboratory animal), in need of
XX osteoinduction, such as the site in need of a bone graft in a subject, a
XX segmental bone gap, a bone void or a non-union fracture. This sequence

CC represents a thrombin peptide derivative obtained from a serine esterase
CC that can stimulate or activate the non-proteolytically activated thrombin
CC receptor
XX
SQ Sequence 14 AA;

Query Match 94.4%; Score 67; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.014; 0; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGDACXGDSGGPXV 14
Db 1 RGDACXGDSGGPXV 14

RESULT 2
AAE20158
ID AAE20158 standard; peptide; 14 AA.
XX AC AAE20158;
XX OS Homo sapiens.
XX DT 18-JUN-2002 (first entry)
XX DE Human thrombin peptide derivative #1.
XX KW Cartilage growth; cartilage repair; arthritic joint; traumatic injury;
KW non-proteolytically activated thrombin receptor; NPAR; chondrocyte;
KW therapy; implantation; thrombin peptide; human.
XX OS Homo sapiens.

XX FH Key Location/Qualifiers
FT Misc-difference 6 /label= Glu, Gln
FT FT Misc-difference 13
FT FT /label= Phe, Met, Leu, His, Val
XX PN WO200207748-A2.
XX PD 31-JAN-2002.

XX PF 19-JUL-2001; 2001WO-US022668.
XX PR 20-JUL-2000; 2000US-0219800P.
XX PA (TEXA) UNIV TEXAS SYSTEM.
XX PI Carney DH, Crowther RS, Stiernberg J, Bergmann J;

XX DR WPI; 2002-268953/31.
XX PT Stimulating growth and repair of cartilage, useful for treating e.g.
XX arthritis, by local administration of an agonist of non-proteolytically
XX activated thrombin receptor.
XX PS Claim 11; Page 25; 28pp; English.

XX CC The invention relates to a method of stimulating growth and repair of
XX cartilage. The method involves administering to the site, an agonist of
XX non-proteolytically activated thrombin receptor (NPAR). The method is
XX used in human or veterinary medicine for the treatment of arthritic
XX joints and damage/loss of cartilage caused by traumatic injury. Also
XX chondrocytes may be cultured in presence of NPAR agonist to provide cells
XX for implantation at sites requiring growth/repair of cartilage. The
XX present sequence is human thrombin peptide derivative which serves as a
XX NPAR agonist

XX SQ Sequence 14 AA;
Query Match 94.4%; Score 67; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.014; 0; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGDACXGDSGGPXV 14
Db 1 RGDACXGDSGGPXV 14

RESULT 3
ABB80264
ID ABB80264 standard; peptide; 14 AA.
XX AC ABB80264;
XX DT 18-DEC-2003 (first entry)
XX DE Thrombin peptide derivative #2.

XX KW Serine esterase; conserved domain; thrombin peptide; stimulation; bone;
KW cartilage; growth; repair; bone graft; segmental gap; bone void;
KW non-union fracture; arthritic joint; arthritis; damage; traumatic injury;
KW culture; chondrocyte; joint bio mechanics; osteoarthritis.

XX OS Mammal sp.
XX FH Key Location/Qualifiers
FT Misc-difference 6 /label= Glu, Gln
FT FT Misc-difference 13 /label= Phe, Met, Leu, His, Val
XX PN WO2003061690-A1.
XX PD 31-JUL-2003.
XX PF 17-JAN-2002; 2002WO-US001451.
XX PR 17-JAN-2002; 2002WO-US001451.

XX PA (TEXA) UNIV TEXAS SYSTEM.
XX PI Carney DH, Crowther RS, Simmons DJ, Yang J, Redin WR;
PI Stiernberg J, Bergmann J;
XX DR WPI; 2003-721552/68.
XX PT Stimulation of bone growth and cartilage formation in e.g. bone graft and
XX arthritic joints involves administration of a thrombin derivative
XX peptide.
XX PS Disclosure; Page 9; Opp; English.

XX CC The sequences given in ABB80263-65 represent thrombin derivative peptides
XX of the invention. The thrombin derivative peptides of the invention have
XX the formula: Asp-Ala-R, where R is a serine esterase conserved domain.
XX These peptides are used for stimulating bone growth and cartilage growth
XX or repair in e.g. bone graft, segmental gap in a bone, bone void, at a
XX non-union fracture, arthritic joints, and sites treated for cartilage
XX damage or loss due to traumatic injury, and for culturing chondrocytes in
XX vitro. The thrombin derivative peptide improves the quality of repair
XX tissue, leads to more durable and functional restoration of joint bio
XX mechanics, reduces the incidence of osteoarthritis in patients suffering
XX from traumatic cartilage injuries and accelerates the rate of normal
XX fracture healing in fracture or small gap defects

XX SQ Sequence 14 AA;

Query Match 94.4%; Score 67; DB 7; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGDACXGDSGGPXV 14
Db 1 RGDACXGDSGGPXV 14

RESULT 4
AAE17240
ID AAE17240 standard; peptide; 14 AA.
XX
AC AAE17240;
XX
DT 18-APR-2002 (first entry)
XX
DE Human transmembrane serine protease-related type I fibronectin domain #1.
XX
KW Transmembrane serine protease; gene therapy; metastasis; tumour;
KW chronic obstructive pulmonary disease; COPD; angiogenesis; inflammation;
KW atherosclerosis; neurodegenerative disease; neuroprotective; cytostatic;
KW pathogenic infection; antiinflammatory; antiarteriosclerotic;
KW antibacterial; type I fibronectin domain.
XX
OS Unidentified.
XX
PN WO200196538-A2.
XX
PD 20-DEC-2001.
XX
PF 12-JUN-2001; 2001WO-EP006618.
XX
PR 13-JUN-2000; 2000US-0211224P.
XX
PR 13-APR-2001; 2001US-0283353P.
XX
PR 16-APR-2001; 2001US-0283648P.
XX
PA (FARB) BAYER AG.
XX
PI Xiao Y, Gedrich R;
XX
PI Xiao Y;
XX
DR WPI; 2002-098065/13.
XX
PT Novel isolated polynucleotide encoding transmembrane serine protease
PT polypeptide, for treating chronic obstructive pulmonary disease, tumor
PT angiogenesis, inflammation, atherosclerosis and neurodegenerative
PT disease.
XX
PS Disclosure; Fig 3; 120pp; English.
XX
CC The present invention relates to an isolated polynucleotide encoding a
CC transmembrane serine protease polypeptide. Transmembrane serine protease
CC gene is useful in gene therapy. The invention also relates to a
CC pharmaceutical composition which is useful for modulating the activity of
CC transmembrane serine protease in a disease, such as chronic obstructive
CC pulmonary disease (COPD), metastasis of malignant cells, tumour
CC angiogenesis, inflammation, atherosclerosis, a neurodegenerative disease
CC or pathogenic infection. Transmembrane serine protease is useful as a
CC bait protein in a two-hybrid or three-hybrid assay. The polypeptide is
CC useful for generating antibodies against it and in various assay systems.
CC The present sequence is a human transmembrane serine protease-related
CC type I fibronectin domain
XX
SQ Sequence 14 AA;
Query Match 74.6%; Score 53; DB 5; Length 14;
Best Local Similarity 75.0%; Pred. No. 1.1;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 3 DACKGDSGGPXV 14
|:|:|:|:|:|:|
Db 2 DSCQDGGGGLV 13
RESULT 5
AAE18999
ID AAE18999 standard; peptide; 14 AA.
XX
AC AAE18999;
XX
XX 21-MAY-2002 (first entry)
DT

DE Human matrilysin-like serine protease related fibronectin domain #1.
XX
KW Human; matrilysin-like serine protease; cardiovascular; antiinflammatory;
KW cytostatic; chronic obstructive pulmonary disease; pulmonary; vulvar;
KW viricide; nervous system disorder; extracellular matrix degradation; wound;
KW antimicrobial; neuroprotective; cancer; cardiovascular disorder; melanoma;
KW adenocarcinoma; neurodegenerative disease; Alzheimer's disease; melanoma;
KW Genstmann-Straussler Syndrome; Creutzfeldt-Jakob disease; scrapie;
KW Parkinson's disease; enzyme; type I fibronectin domain.
XX
OS Unidentified.
XX
PN WO200208392-A2.
XX
PD 31-JAN-2002.
XX
PF 16-JUL-2001; 2001WO-EP008182.
XX
PR 25-JUL-2000; 2000US-0220807P.
XX
PR 02-APR-2001; 2001US-0280109P.
XX
PA (FARB) BAYER AG.
XX
PI Xiao Y;
XX
DR WPI; 2002-195871/25.
XX
PT New matrilysin-like serine protease proteins and polynucleotides, useful
PT for treating matrilysin-like serine protease dysfunction related
PT diseases, e.g. cancer, pulmonary disease, wounds, inflammation or viral
PT infections.
XX
PS Disclosure; Fig 9; 140pp; English.
XX
CC The patent discloses novel matrilysin-like serine protease proteins and
CC their corresponding polynucleotides. The invention further relates to
CC reagents and methods of regulating human matrilysin-like serine protease
CC activity. Pharmaceutical compositions comprising the reagents of the
CC invention are useful for modulating the activity of a matrilysin-like
CC serine protease in a disease. The reagents are also useful for treating
CC or ameliorating matrilysin-like serine protease dysfunction related
CC diseases such as cancer, chronic obstructive pulmonary disease, central
CC or peripheral nervous system disorder and cardiovascular disorder. The
CC human matrilysin-like serine protease gene provides a therapeutic target
CC to decrease extracellular matrix degradation, in particular for treating
CC or preventing metastatic cancer, e.g. adenocarcinoma, melanoma, cancers
CC of the adrenal gland, bladder, bone breast, cervix, gall bladder, liver,
CC lung, ovary, pancreas, prostate, testis or uterus. Sequences of the
CC invention are also useful for treating neurodegenerative diseases (e.g.,
CC Alzheimer's disease, Parkinson's disease), wounds, inflammation or viral
CC infections. Matrilysin-like serine protease activity can be used to
CC degrade, prion protein amyloid plaques of Genstmann-Straussler Syndrome,
CC Creutzfeldt-Jakob disease and Scrapie. The present sequence is human
CC matrilysin-like serine protease related type I fibronectin domain
XX
SQ Sequence 14 AA;
Query Match 74.6%; Score 53; DB 5; Length 14;
Best Local Similarity 75.0%; Pred. No. 1.1;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 3 DACKGDSGGPXV 14
|:|:|:|:|:|:|
Db 2 DSCQDGGGGLV 13
RESULT 6
AAU80522
ID AAU80522 standard; protein; 14 AA.
XX
AC AAU80522;
XX
DT 12-MAR-2002 (first entry)

PA (EIDG-) EIDGENOESSISCHE TECH HOCHSCHULE ZUERICH.

XX Neri D, Tarli L, Viti F, Birchler M;
 XX WPI; 2000-039074/03.
 XX Fibrinectin ED-B domain epitope specific antibodies and conjugate
 PT antibodies.
 XX Claim 10; Page 38; 59pp; English.
 XX The present sequence represents a linker component of a modified human
 CC scFv antibody which has specific affinity for a characteristic epitope of
 CC the ED-B domain of fibrinectin. The affinity of the antibody for this
 CC epitope was improved by introducing a number of mutations in the
 CC complementarity determining region (CDR) residues located at the
 CC periphery of the binding site. The improved antibody is used for rapid
 CC targeting markers of angiogenesis, for detecting diseases characterized
 CC by vascular proliferation, such as diabetic retinopathy, age-related
 CC macular degeneration or tumours. The antibody localizes the respective
 CC tissue within 3 to 4 hours after injection. It is used in
 CC immunocytographic detection of angiogenesis and for diagnosis and
 CC therapy of tumours and diseases characterized by vascular proliferation.
 CC The antibody can be conjugated to a molecule which induces blood
 CC coagulation and blood vessel occlusion. These conjugates are used in the
 CC preparation of injectable compositions for the treatment of angiogenesis-
 CC related pathologies, especially caused by or associated with ocular
 CC angiogenesis.

XX Sequence 14 AA;

Query Match 45.1%; Score 32; DB 3; Length 14;
 Best Local Similarity 60.0%; Pred. No. 7.7e+02;
 Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GDACXGDSGG 11
 |||
 DB 1 GDGSGGSGG 10

RESULT 9

AAE08818
 ID AAE08818 standard; protein; 14 AA.

AC AAE08818;

DT 19-NOV-2001 (first entry)

DE Synthetic peptide linker for constructing ScFv L19 antibody.

XX ScFv; single-chain variable antibody fragment; cancer; cytotoxic;
 KW coagulant; ED-B domain; fibrinectin; tumor; ocular disorder; psoriasis;
 KW vascular proliferation; rheumatoid arthritis; blood vessel occlusion;
 KW angiogenesis; blood coagulation.

OS Synthetic.

XX WO200162800-A1.

PN 30-AUG-2001.

PF 23-FEB-2001; 2001WO-EP002062.

XX 24-FEB-2000; 2000US-00512082.

PA (EIDG-) EIDGENOESSISCHE TECH HOCHSCHULE ZUERICH.

XX Neri D, Tarli L, Viti F, Birchler M;

XX WPI; 2001-541701/60.

XX An antibody, with specific affinity for a characteristic epitope of the
 PT ED-B domain of fibrinectin for the treatment of diseases characterized by

PT vascular proliferation.

XX Claim 10; Page 36; 73pp; English.

XX The invention relates to an antibody with specific affinity for a
 CC characteristic epitope of the ED-B domain of fibrinectin, where the
 CC antibody has improved affinity to ED-B. The invention also relates to
 CC conjugates comprising antibodies with a suitable photoactive molecule
 CC useful in the detection and/or coagulation of blood vessels. An antibody
 CC with improved affinity to the ED-B domain is useful for diagnosis and
 CC therapy of tumours and diseases characterised by vascular proliferation,
 CC cancer, rheumatoid arthritis, neo-vasculature associated ocular disorders
 CC and psoriasis. Treatment of angiogenesis related pathologies comprises
 CC the injection of conjugates comprising antibody and a molecule capable of
 CC inducing blood coagulation and blood vessel occlusion. The present
 CC sequence is a peptide linker used for constructing single-chain variable
 CC antibody fragment (scFv) L19 antibody related to the invention

XX Sequence 14 AA;

Query Match 45.1%; Score 32; DB 4; Length 14;
 Best Local Similarity 60.0%; Pred. No. 7.7e+02;
 Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GDACXGDSGG 11
 |||
 DB 1 GDGSGGSGG 10

RESULT 10

AAE29569

ID AAE29569 standard; peptide; 14 AA.

AC AAE29569;

DT 27-JAN-2003 (first entry)

DE Metallopeptide #13 used for Prion disease treatment.

XX Metallopeptide; nontropic; amyloid beta-protein; Alzheimer's disease; AD;
 KW Prion's disease; oxytocin; angiotensin; vasopressin; neuroprotective;
 KW therapy.

XX Unidentified.

XX Key Location/Qualifiers

FT Misc-difference 3
 FT /label= Pro, Gly, Ala

XX WO200264734-A2.

XX 22-AUG-2002.

XX 19-DEC-2001; 2001WO-US0500075.

XX 19-DEC-2000; 2000US-0256842P.

XX 11-JUL-2001; 2001US-0304835P.

XX 04-OCT-2001; 2001US-0327835P.

XX (PALA-) PALATIN TECHNOLOGIES INC.

XX Sharma SD, Shi Y;

XX WPI; 2002-740699/80.

XX Determining secondary structure binding to desired targets within parent
 PT polypeptides that bind to targets, by constructing and complexing
 PT peptides to metal ions to form metallopeptides and screening the
 PT metallopeptides.

XX Example 3; Page 140; 165pp; English.

XX The invention relates to a method for identification and determination of

CC target-specific folding sites in peptides and proteins. The invention
 CC also relates to a method for determining a secondary structure binding to
 CC desired targets within parent polypeptides that bind to targets, by
 CC constructing and complexing peptides to metal ions to form
 CC metalloprotein and screening the metalloprotein. The method is useful
 CC for determining secondary structure binding to desired target within
 CC parent polypeptide with primary structure that binds to the target, where
 CC the target of interest is a receptor, antibody, toxin, enzyme, hormone,
 CC nucleic acid, intracellular protein domain of biological relevance or
 CC extracellular protein domain of biological relevance. A library of
 CC amyloid beta-protein related peptides is useful for the treatment of
 CC Alzheimer's disease (AD). A library of peptides targeting vasopressin,
 CC oxytocin or angiotensin receptor is useful for treating Prion's disease.
 CC The present sequence is a metalloprotein used for Prion disease
 CC treatment. This peptide is used to illustrate the method of the invention
 XX
 SQ Sequence 14 AA;
 Query Match 45.1%; Score 32; DB 5; Length 14;
 Best Local Similarity 58.3%; Pred. No. 7.7e+02;
 Matches 7; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 3 DACKGDSGGPXV 14
 DB 1 DACKAAPAGPAV 12
 RESULT 11
 AAE29631
 ID AAE29631 standard; peptide; 14 AA.
 AC AAE29631;
 DT 27-JAN-2003 (first entry)
 DE Metalloprotein #16 used for Prion disease treatment.
 KW Metalloprotein; nontropic; amyloid beta-protein; Alzheimer's disease;
 KW Prion's disease; oxytocin; angiotensin; vasopressin; neuroprotective; AD;
 KW therapy.
 OS Unidentified.
 PH Key Location/Qualifiers
 FT Misc-difference 4 /label= Pro, Gly, Ala
 FT WO200264734-A2.
 XX 22-AUG-2002.
 XX 19-DEC-2001; 2001WO-US050075.
 XX 19-DEC-2000; 2000US-0256842P.
 XX 11-JUL-2001; 2001US-0304835P.
 XX 04-OCT-2001; 2001US-0327835P.
 XX (PALA-) PALATIN TECHNOLOGIES INC.
 XX Sharma SD, Shi Y;
 XX WPI; 2002-740699/80.
 XX Determining secondary structure binding to desired targets within parent
 XX polypeptides that bind to targets, by constructing and complexing
 XX peptides to metal ions to form metalloprotein and screening the
 XX metalloprotein.
 XX Example 3; Page 157; 165pp; English.
 XX The invention relates to a method for identification and determination of
 XX target-specific folding sites in peptides and proteins. The invention
 CC also relates to a method for determining a secondary structure binding to

CC desired targets within parent polypeptides that bind to targets, by
 CC constructing and complexing peptides to metal ions to form
 CC metalloprotein and screening the metalloprotein. The method is useful
 CC for determining secondary structure binding to desired target within
 CC parent polypeptide with primary structure that binds to the target, where
 CC the target of interest is a receptor, antibody, toxin, enzyme, hormone,
 CC nucleic acid, intracellular protein domain of biological relevance or
 CC extracellular protein domain of biological relevance. A library of
 CC amyloid beta-protein related peptides is useful for the treatment of
 CC Alzheimer's disease (AD). A library of peptides targeting vasopressin,
 CC oxytocin or angiotensin receptor is useful for treating Prion's disease.
 CC The present sequence is a metalloprotein used for Prion disease
 CC treatment. This peptide is used to illustrate the method of the invention
 XX
 SQ Sequence 14 AA;
 Query Match 45.1%; Score 32; DB 5; Length 14;
 Best Local Similarity 58.3%; Pred. No. 7.7e+02;
 Matches 7; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 3 DACKGDSGGPXV 14
 DB 1 DACKAAPAGPAV 12
 RESULT 12
 AAR93584
 ID AAR93584 standard; peptide; 14 AA.
 AC AAR93584;
 DT 08-OCT-1996 (first entry)
 DE Dopamine receptor isoform D5 peptide analogue (aa: 23-35-Cys36).
 KW Dopamine; identification; neurotransmitter; diagnosis; analogue;
 KW isoform-specific antibody; receptor; distinguish; identification;
 KW Parkinson's disease; Alzheimer's disease; neurological.
 OS Synthetic.
 PH Key Location/Qualifiers
 FT Misc-difference 1 /note= "opt. acetylated"
 FT WO9606856-A1.
 XX 07-MAR-1996.
 XX 30-AUG-1995; 95WO-US011127.
 XX 31-AUG-1994; 94US-00298600.
 XX (WEBB/) WEBBER R.
 XX Webber R;
 XX WPI; 1996-160304/16.
 XX Peptide analogues of different dopamine receptor isoform(s) - also
 XX antibodies raised against them, useful in drug development and diagnosis,
 XX e.g. of Parkinson's disease.
 XX Claim 1; Fig 5c; 56pp; English.
 XX AAR93582-R93586 are peptide analogues of the dopamine receptor isoform
 XX D5. The analogues correspond to regions that are variable between the
 XX five different isoforms, D1, D2, D3, D4 and D5 and as such are specific
 XX for the particular isoform. The peptides or antibodies raised against
 XX them are useful in developing drugs for the treatment of and diagnosis of
 XX disorders related to the dopamine receptor e.g. Parkinson's disease and
 XX Alzheimer's disease

[illegible]

XX ABB56805;
AC
XX
DT 05-MAR-2002 (first entry)
XX
DE Human SNP related amino acid sequence SEQ ID NO:1370.
XX
KW Human; single nucleotide polymorphism; SNP; polymorphism; cytostatic;
KW immunosuppressive; antiinflammatory; neuroprotective; antimicrobial;
KW autoimmune disease; inflammation; cancer; nervous system disease;
KW infection; polymorphic protein.
XX
OS Homo sapiens.
XX
PN WO200138586-A2.
XX
PD 31-MAY-2001.
XX
PF 22-NOV-2000; 2000WO-US032311.
XX
PR 24-NOV-1999; 99US-0167383P.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkets RA, Leach M;
XX
XX WPI; 2001-355949/37.
XX
DR Isolated human nucleic acids comprising one or more single nucleotide
PT polymorphisms, useful for treating a subject suffering from a pathology,
PT e.g. autoimmune diseases, ascribed to the presence of a sequence
PT polymorphism.
XX
PS Claim 1; Page 650; 67app; English.
XX
XX ABL00010 to ABL01104 represent human nucleic acid oligonucleotides
CC comprising one or more single nucleotide polymorphisms (SNPs). ABB56531
CC to ABB56903 represent human peptides encoded by some of the SNP
CC oligonucleotides. The sequences from the present invention can have
CC immunosuppressive, cytostatic, antiinflammatory, neuroprotective and
CC antimicrobial activities. Nucleic acids, polypeptides, oligonucleotides
CC and antibodies from the present invention can be used for treating a
CC subject suffering from, at risk for, or suspected of, suffering from a
CC pathology ascribed to the presence of a sequence polymorphism. The
CC pathology may be autoimmune diseases, inflammation, cancer, diseases of
CC the nervous system, and infection by pathogenic microorganisms. The SNPs
CC are also useful for determining which forms of a characterised
CC polymorphism are present in individuals. The antibodies may be used in
CC the detection, quantitation and/or cellular or tissue localisation of a
CC polymorphic protein (e.g., for use in measuring levels of the polymorphic
CC protein within appropriate physiological samples)
XX
SQ Sequence 14 AA;
Query Match 42.3%; Score 30; DB 4; Length 14;
Best Local Similarity 83.3%; Pred. No. 1.4e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 5 CXGDSG 10
Db 1 CQGDSD 6
Search completed: February 26, 2004, 09:40:43
Job time : 55 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

protein - protein search, using sw model

n on: February 26, 2004, 09:41:42 ; Search time 33 Seconds
      (without alignments)
      89.580 Million cell updates/sec

File: US-09-909-348-4
Perfect score: 71
Sequence: 1 RGDACXGDSGGPXV 14

oring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

arched: 803742 seqs, 211153259 residues

total number of hits satisfying chosen parameters: 6887

Minimum DB seq length: 14
Maximum DB seq length: 14

at-processing: Minimum Match 0%
                Maximum Match 100%
                Listing first 45 summaries

Database : Published Applications AA.*

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SUMMARIES

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1	67	94.4	14	9	US-09-309-123-4
2	67	94.4	14	9	US-10-050-692-4
3	67	94.4	14	13	US-10-050-688-4
4	52	73.2	14	9	US-09-885-441-6
5	32	45.1	14	10	US-09-300-425B-20
6	32	45.1	14	14	US-10-321-558-31
7	30	42.3	14	15	US-10-341-993-8
8	27	38.0	14	10	US-09-880-748-3215
9	25	35.2	14	9	US-09-815-837-109
10	25	35.2	14	10	US-09-852-455-34
11	25	35.2	14	10	US-09-852-455-35
12	25	35.2	14	10	US-09-852-455-36
13	25	35.2	14	10	US-09-852-455-37
14	25	35.2	14	10	US-09-852-455-38
15	25	35.2	14	10	US-09-880-748-3218
					Sequence 4, Appli
					Sequence 4, Appli
					Sequence 4, Appli
					Sequence 6, Appli
					Sequence 20, Appl
					Sequence 31, Appl
					Sequence 8, Appli
					Sequence 3215, Ap
					Sequence 109, App
					Sequence 35, Appl
					Sequence 36, Appl
					Sequence 37, Appl
					Sequence 38, Appl
					Sequence 3218, Ap


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;
; FEATURE:
; OTHER INFORMATION: peptide fragment of thrombin
;
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (6)...(6)
; OTHER INFORMATION: Xaa = Glu or Gln
;
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (13)...(13)
; OTHER INFORMATION: Xaa = Phe, Met, Leu, His or Val
;
; US-10-050-688-4
;
; Query Match          94.4%; Score 67; DB 13; Length 14;
; Best Local Similarity 100.0%; Pred.No. 0.00066;
; Matches 14; Conservative 0; Mismatches 0; Indels
;
; QY      1  RGDACKGDSGGPXV 14
;         |||||
;         |||||
;         |||||
;         |||||
;         |||||
;
; Db       1  RGDCKXGDSGGPXV 14
;
;
; RESULT 4
; US-09-885-441-6
; Sequence 6, Application US/09885441
; Patent No. US20020146407A1
;
; GENERAL INFORMATION:
; APPLICANT: Xiao Yonghong
; TITLE OF INVENTION: Regulation of Human Eosinophil Serine
; TITLE OF INVENTION: Protease-1-Like Enzyme
; FILE REFERENCE: 04974.00512
; CURRENT APPLICATION NUMBER: US/09/885.441
; CURRENT FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/212,844
; PRIOR FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: US 60/244,171
; PRIOR FILING DATE: 2000-10-31
; PRIOR APPLICATION NUMBER: US 60/279,766
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: PCT/
; PRIOR FILING DATE: 2001-06-20
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
;
; FEATURE:
; OTHER INFORMATION: BLOCKS domain
;
; US-09-885-441-6
;
; Query Match          73.2%; Score 52; DB 9; Length 14;
; Best Local Similarity 75.0%; Pred.No. 0.13;
; Matches 9; Conservative 0; Mismatches 3; Indels
;
; QY      3  DACKGDSGGPXV 14
;         |||||
;         |||||
;         |||||
;
; Db       2  DTCKGDSGGPLV 13
;
;
; RESULT 5
; US-09-300-425B-20
; Sequence 20, Application US/09300425B
; Publication NO. US20030045681A1
;
; GENERAL INFORMATION:
; APPLICANT: NERI, Dario
; APPLICANT: TALI, Lorenzo
; APPLICANT: VITI, Francesca
; APPLICANT: BIRCHLER, Manfred
; TITLE OF INVENTION: SPECIFIC BINDING MOLECULES FOR SCINTIGRAPHY
; TITLE OF INVENTION: CONTAINING THEM AND THERAPEUTIC METHOD
; TITLE OF INVENTION: ANGIOGENESIS
; FILE REFERENCE: SCH-1733P1
; CURRENT APPLICATION NUMBER: US/09/300.425B

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; CURRENT FILING DATE: 1999-04-28
 ; PRIOR APPLICATION NUMBER: 09/075,338
 ; PRIOR FILING DATE: 1998-05-11
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: Patent In Ver. 2.1
 ; SEQ ID NO 20
 ; LENGTH: 14
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: antibody linker
 US-09-300-425B-20

Query Match 45.1%; Score 32; DB 10; Length 14;
 Best Local Similarity 60.0%; Pred. No. 1.5e+02;
 Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GDACXGDSGG 11
 Db 1 GDGSGSGG 10

RESULT 6
 US-10-321-558-31
 ; Sequence 31, Application US/10321558
 ; Publication No. US2003017663A1
 ; GENERAL INFORMATION:
 ; APPLICANT: NERI, DARIO
 ; APPLICANT: TARLI, LORENZO
 ; APPLICANT: VITI, FRANCESCA
 ; APPLICANT: BIRCHLER, MANFRED
 ; TITLE OF INVENTION: SPECIFIC BINDING MOLECULES FOR SCINTIGRAPHY
 ; FILE REFERENCE: NOTAR-1 C1
 ; CURRENT APPLICATION NUMBER: US/10/321,558
 ; CURRENT FILING DATE: 2002-12-18
 ; PRIOR APPLICATION NUMBER: 09/512,082
 ; PRIOR FILING DATE: 2000-02-24
 ; PRIOR APPLICATION NUMBER: 09/300,425
 ; PRIOR FILING DATE: 1999-04-28
 ; PRIOR APPLICATION NUMBER: 09/075,338
 ; PRIOR FILING DATE: 1998-05-11
 ; NUMBER OF SEQ ID NOS: 32
 ; SOFTWARE: Patent In Ver. 2.1
 ; SEQ ID NO 31
 ; LENGTH: 14
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 ; OTHER INFORMATION: linker sequence
 US-10-321-558-31

Query Match 45.1%; Score 32; DB 14; Length 14;
 Best Local Similarity 60.0%; Pred. No. 1.5e+02;
 Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GDACXGDSGG 11
 Db 1 GDGSGSGG 10

RESULT 7
 US-10-341-979-8
 ; Sequence 8, Application US/10341979
 ; Publication No. US20040002128A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hong Kong University of Science & Technology
 ; APPLICANT: Chang, Donald Choy
 ; APPLICANT: Luo, Qian Kathy
 ; TITLE OF INVENTION: GFP-BASED METHODS FOR DETECTING APOPTOSIS
 ; FILE REFERENCE: 32144183-1
 ; CURRENT APPLICATION NUMBER: US/10/341,979
 ; CURRENT FILING DATE: 2003-01-11

; NUMBER OF SEQ ID NOS: 20
 ; SOFTWARE: Patent In version 3.1
 ; SEQ ID NO 8
 ; LENGTH: 14
 ; TYPE: PRT
 ; ORGANISM: mammalian
 US-10-341-979-8

Query Match 42.3%; Score 30; DB 15; Length 14;
 Best Local Similarity 60.0%; Pred. No. 3.1e+02;
 Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GDACXGDSGG 11
 Db 5 GDEVGGSGG 14

RESULT 8
 US-09-880-748-3215
 ; Sequence 3215, Application US/09880748
 ; Publication No. US20030059937A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruben et al.
 ; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
 ; FILE REFERENCE: PF523
 ; CURRENT APPLICATION NUMBER: US/09/880,748
 ; CURRENT FILING DATE: 2001-06-15
 ; PRIOR APPLICATION NUMBER: 60/212,210
 ; PRIOR FILING DATE: 2000-06-15
 ; PRIOR APPLICATION NUMBER: 60/240,816
 ; PRIOR FILING DATE: 2000-10-17
 ; PRIOR APPLICATION NUMBER: 60/276,248
 ; PRIOR FILING DATE: 2001-03-16
 ; PRIOR APPLICATION NUMBER: 60/277,379
 ; PRIOR FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: 60/293,499
 ; PRIOR FILING DATE: 2001-05-25
 ; NUMBER OF SEQ ID NOS: 3239
 ; SOFTWARE: Patent In Ver. 2.0
 ; SEQ ID NO 3215
 ; LENGTH: 14
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-880-748-3215

Query Match 38.0%; Score 27; DB 10; Length 14;
 Best Local Similarity 83.3%; Pred. No. 8.9e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GDGSGP 12
 Db 7 GDGSGP 12

RESULT 9
 US-09-815-837-109
 ; Sequence 109, Application US/09815837
 ; Patent No. US20020082411A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Carter, Darrick
 ; APPLICANT: Zhu, Shirley
 ; APPLICANT: Atimilli, Subhashini
 ; APPLICANT: Wang, Aijun
 ; APPLICANT: Corixa Corporation
 ; TITLE OF INVENTION: Immune Mediators and Related Methods
 ; FILE REFERENCE: 014058-005670US
 ; CURRENT APPLICATION NUMBER: US/09/815,837
 ; CURRENT FILING DATE: 2001-03-22
 ; PRIOR APPLICATION NUMBER: US 60/191,274
 ; PRIOR FILING DATE: 2000-03-22
 ; PRIOR APPLICATION NUMBER: US 60/204,249
 ; PRIOR FILING DATE: 2000-05-15
 ; PRIOR APPLICATION NUMBER: US 60/264,003

; PRIOR FILING DATE: 2001-01-23
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 109
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: downstream
; OTHER INFORMATION: linker for C0580 and C0587
US-09-815-837-109

Query Match 35.2%; Score 25; DB 9; Length 14;
Best Local Similarity 66.7%; Pred. No. 1.8e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 GDSGGP 12
|: |||
Db 7 GSGGGP 12

RESULT 10
US-09-852-455-34
; Sequence 34, Application US/09852455
; Publication No. US20030054348A1
; GENERAL INFORMATION:
; APPLICANT: BLUME, ARTHUR J.
; APPLICANT: GOLDSTEIN, NEIL
; APPLICANT: PILLUTA, RENUKA
; APPLICANT: HSIAO, KU-CHUAN
; APPLICANT: PRENDERGAST, JOHN
; TITLE OF INVENTION: METHODS OF IDENTIFYING THE ACTIVITY OF GENE PRODUCTS
; FILE REFERENCE: 2598-4004US1
; CURRENT APPLICATION NUMBER: US/09/852,455
; CURRENT FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: 60/202,912
; PRIOR FILING DATE: 2000-05-09
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 34
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Bos taurus
US-09-852-455-34

Query Match 35.2%; Score 25; DB 10; Length 14;
Best Local Similarity 66.7%; Pred. No. 1.8e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 GDSGGP 12
|: |||
Db 1 GELGGP 6

RESULT 11
US-09-852-455-35
; Sequence 35, Application US/09852455
; Publication No. US20030054348A1
; GENERAL INFORMATION:
; APPLICANT: BLUME, ARTHUR J.
; APPLICANT: GOLDSTEIN, NEIL
; APPLICANT: PILLUTA, RENUKA
; APPLICANT: HSIAO, KU-CHUAN
; APPLICANT: PRENDERGAST, JOHN
; TITLE OF INVENTION: METHODS OF IDENTIFYING THE ACTIVITY OF GENE PRODUCTS
; FILE REFERENCE: 2598-4004US1
; CURRENT APPLICATION NUMBER: US/09/852,455
; CURRENT FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: 60/202,912
; PRIOR FILING DATE: 2000-05-09
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 35

; LENGTH: 14
; TYPE: PRT
; ORGANISM: Cavia porcellus
US-09-852-455-35

Query Match 35.2%; Score 25; DB 10; Length 14;
Best Local Similarity 66.7%; Pred. No. 1.8e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 GDSGGP 12
|: |||
Db 1 GELGGP 6

RESULT 12
US-09-852-455-36
; Sequence 36, Application US/09852455
; Publication No. US20030054348A1
; GENERAL INFORMATION:
; APPLICANT: BLUME, ARTHUR J.
; APPLICANT: GOLDSTEIN, NEIL
; APPLICANT: PILLUTA, RENUKA
; APPLICANT: HSIAO, KU-CHUAN
; APPLICANT: PRENDERGAST, JOHN
; TITLE OF INVENTION: METHODS OF IDENTIFYING THE ACTIVITY OF GENE PRODUCTS
; FILE REFERENCE: 2598-4004US1
; CURRENT APPLICATION NUMBER: US/09/852,455
; CURRENT FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: 60/202,912
; PRIOR FILING DATE: 2000-05-09
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 36
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-852-455-36

Query Match 35.2%; Score 25; DB 10; Length 14;
Best Local Similarity 66.7%; Pred. No. 1.8e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 GDSGGP 12
|: |||
Db 1 GELGGP 6

RESULT 13
US-09-852-455-37
; Sequence 37, Application US/09852455
; Publication No. US20030054348A1
; GENERAL INFORMATION:
; APPLICANT: BLUME, ARTHUR J.
; APPLICANT: GOLDSTEIN, NEIL
; APPLICANT: PILLUTA, RENUKA
; APPLICANT: HSIAO, KU-CHUAN
; APPLICANT: PRENDERGAST, JOHN
; TITLE OF INVENTION: METHODS OF IDENTIFYING THE ACTIVITY OF GENE PRODUCTS
; FILE REFERENCE: 2598-4004US1
; CURRENT APPLICATION NUMBER: US/09/852,455
; CURRENT FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: 60/202,912
; PRIOR FILING DATE: 2000-05-09
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 37
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-852-455-37

Query Match 35.2%; Score 25; DB 10; Length 14;
Best Local Similarity 66.7%; Pred. No. 1.8e+03;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 GDSGGP 12
| : |||
Db 1 GELGGP 6

Db 2 RPDADYGDYG 11

Search completed: February 26, 2004, 09:47:14
Job time : 34 secs

RESULT 14
US-09-852-455-38
; Sequence 38, Application US/09852455
; Publication No. US20030054348A1
; GENERAL INFORMATION:
; APPLICANT: BLUME, ARTHUR J.
; APPLICANT: GOLDSTEIN, NEIL
; APPLICANT: PILLIUTA, RENUKA
; APPLICANT: HSIAO, KU-CHUAN
; APPLICANT: PRENDERGAST, JOHN
; TITLE OF INVENTION: METHODS OF IDENTIFYING THE ACTIVITY OF GENE PRODUCTS
; FILE REFERENCE: 2598-4004US1
; CURRENT APPLICATION NUMBER: US/09/852,455
; CURRENT FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: 60/202,912
; PRIOR FILING DATE: 2000-05-09
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Felis catus
US-09-852-455-38

Query Match 35.2%; Score 25; DB 10; Length 14;
Best Local Similarity 66.7%; Pred. No. 1.8e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 GDSGGP 12
| : |||
Db 1 GELGGP 6

RESULT 15
US-09-880-748-3218
; Sequence 3218, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3218
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-3218

Query Match 35.2%; Score 25; DB 10; Length 14;
Best Local Similarity 60.0%; Pred. No. 1.8e+03;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 RGDACXGDSG 10

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 26, 2004, 09:39:42 ; Search time 23 Seconds
(without alignments)
31.425 Million cell updates/sec

Title: US-09-909-348-4

Perfect score: 71

Sequence: 1 RGDACXGDSGGPV 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 8296

Minimum DB seq length: 14

Maximum DB seq length: 14

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 3: /cgn2_6/ptodata/2/iaa/6A.COMB.pap:*
- 4: /cgn2_6/ptodata/2/iaa/6B.COMB.pap:*
- 5: /cgn2_6/ptodata/2/iaa/PCTUS.COMB.pap:*
- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	30	42.3	14	3	US-08-981-088-4
3	30	42.3	14	5	PCT-US95-11127-28
4	29	40.8	14	2	US-08-335-832-10
5	29	40.8	14	3	US-09-141-127-4
6	26	36.6	14	1	US-07-994-463A-19
7	26	36.6	14	5	PCT-US91-08328-35
8	26	36.6	14	5	PCT-US91-08328-36
9	26	36.6	14	5	PCT-US91-08328-37
10	26	36.6	14	5	PCT-US91-08328-38
11	25	35.2	14	3	US-08-441-507-43
12	25	35.2	14	3	US-08-441-507-49
13	25	35.2	14	4	US-07-969-875A-43
14	24	33.8	14	2	US-08-487-431-2
15	24	33.8	14	3	US-08-973-625-2
16	24	33.8	14	3	US-09-091-814-8
17	23	32.4	14	1	US-08-172-331B-10
18	23	32.4	14	1	US-08-430-633-5
19	23	32.4	14	1	US-08-471-780C-45
20	23	32.4	14	1	US-08-471-780C-46
21	23	32.4	14	1	US-08-467-282B-45
22	23	32.4	14	1	US-08-467-282B-46
23	23	32.4	14	2	US-08-448-418-101
24	23	32.4	14	2	US-08-471-282A-45
25	23	32.4	14	2	US-08-471-282A-46
26	23	32.4	14	2	US-08-620-694A-5
27	23	32.4	14	2	US-08-466-710C-45

28	23	32.4	14	2	US-08-466-710C-46	Sequence 46, Appl
29	23	32.4	14	2	US-08-936-854-5	Sequence 5, Appl
30	23	32.4	14	2	US-08-564-063-4	Sequence 4, Appl
31	23	32.4	14	2	US-08-656-906-26	Sequence 26, Appl
32	23	32.4	14	3	US-08-468-739C-45	Sequence 45, Appl
33	23	32.4	14	3	US-08-468-739C-46	Sequence 46, Appl
34	23	32.4	14	3	US-09-022-255-5	Sequence 5, Appl
35	23	32.4	14	3	US-09-022-696-5	Sequence 5, Appl
36	23	32.4	14	3	US-09-022-253-5	Sequence 5, Appl
37	23	32.4	14	3	US-09-022-260-5	Sequence 5, Appl
38	23	32.4	14	3	US-09-022-259-5	Sequence 5, Appl
39	23	32.4	14	3	US-09-022-257-5	Sequence 5, Appl
40	23	32.4	14	3	US-09-217-847-26	Sequence 26, Appl
41	23	32.4	14	3	US-09-426-680-4	Sequence 4, Appl
42	23	32.4	14	4	US-09-146-979-101	Sequence 101, App
43	23	32.4	14	4	US-09-125-576B-9	Sequence 9, Appl
44	23	32.4	14	4	US-09-549-679-5	Sequence 5, Appl
45	22	31.0	14	1	US-08-322-962-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-09-631-137C-7
; Sequence 7, Application US/09631137C
; Patent No. 6630572
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; APPLICANT: Glenn, Kevin C.
; TITLE OF INVENTION: Thrombin Derived Polypeptides:
; TITLE OF INVENTION: Compositions and Methods for Use
; FILE REFERENCE: 3033.1001-004
; CURRENT APPLICATION NUMBER: US/09/631,137C
; CURRENT FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 08/538,504
; PRIOR FILING DATE: 1995-09-29
; PRIOR APPLICATION NUMBER: US 08/007,173
; PRIOR FILING DATE: 1993-01-21
; PRIOR APPLICATION NUMBER: US 06/925,201
; PRIOR FILING DATE: 1986-10-31
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fragment of human prothrombin
US-09-631-137C-7

Query Match 94.4%; Score 67; DB 4; Length 14;
Best Local Similarity 85.7%; Pred. No. 0.00062;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qv 1 RGDACXGDSGGPV 14
| | | | | | | | | | | | | | | |
Db 1 RGDACXGDSGGPV 14

RESULT 2
US-08-981-088-4
; Sequence 4, Application US/08981088
; Patent No. 6146824
; GENERAL INFORMATION:
; APPLICANT: BAR-SHAVIT, RACHEL
; TITLE OF INVENTION: ANTI-METASTATIC AND ANTI-ANGIOGENIC
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CLIFF & BERRIDGE, PLC
; STREET: P.O. BOX 19928
; CITY: ALEXANDRIA

```

; STATE: VA
; COUNTRY: USA
; ZIP: 22320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/981,088
; FILING DATE: 27-JAN-1998
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: OLIFF, JAMES A
; REGISTRATION NUMBER: 27,075
; REFERENCE/DOCKET NUMBER: JAO 40455
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)-836-6400
; TELEFAX: (703)-836-2787
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; US-08-981-088-4

Query Match 42.3%; Score 30; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGDAC 5
DB 10 RGDAC 14

RESULT 3
PCT-US95-11127-28
; Sequence 28, Application PC/TUS9511127
; GENERAL INFORMATION:
; APPLICANT: ROBERT WEBBER
; TITLE OF INVENTION: DOPAMINE RECEPTOR PEPTIDES AND
; ANTIODIES
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIELEN, PETERSON & LAMPE
; STREET: 1990 N. CALIFORNIA BOULEVARD, SUITE 720
; CITY: WALNUT CREEK
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 94596
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE 5.25 INCH, 1.2 MB FOR FORMATTED
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/11127
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: NONE
; FILING DATE: NONE
; ATTORNEY/AGENT INFORMATION:
; NAME: THEODORE J. BIELEN, JR.
; REGISTRATION NUMBER: 27,420
; REFERENCE/DOCKET NUMBER: 12068
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 937-1515
; TELEFAX: (510) 937-1529
; INFORMATION FOR SEQ ID NO: 28:

```

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 14
; TYPE: AMINO ACID
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PEPTIDE
; FEATURE:
; NAME/KEY: D5 RECEPTOR (AC-23-35Cys36)
; LOCATION:
; IDENTIFICATION METHOD: AMINO ACID ANALYSIS
; OTHER INFORMATION: DOPAMINE D5 RECEPTOR PEPTIDE
; PCT-US95-11127-28

Query Match 42.3%; Score 30; DB 5; Length 14;
Best Local Similarity 41.7%; Pred. No. 1.7e+02;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 RGDACXGDSGGP 12
DB 1 QGNAVGGGAGAP 12

RESULT 4
US-08-335-832-10
; Sequence 10, Application US/08335832
; Patent No. 5925331
; GENERAL INFORMATION:
; APPLICANT: Dean, Richard T
; TITLE OF INVENTION: Technetium-99m Labeled Peptides for
; THROMBUS IMAGING
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Allegretti, Ltd.
; STREET: 10 South Wacker Drive Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/335,832
; FILING DATE: 05-JAN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5925331nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 92,216-I
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELETYPE: 910-221-5317
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /label= AcM
; OTHER INFORMATION: /note= "This cysteine residue is blocked at the
; OTHER INFORMATION: sidechain sulfur by covalent linkage to an
; OTHER INFORMATION: acetamido group"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 3
; OTHER INFORMATION: /label= AcM
; OTHER INFORMATION: /note= "This cysteine residue is blocked at the

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OTHER INFORMATION: sidechain sulfur by covalent linkage to an
OTHER INFORMATION: acetamido group"
US-08-335-832-10

Query Match 40.8%; Score 29; DB 2; Length 14;
Best Local Similarity 66.7%; Pred. No. 2.4e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 RGDACXGDS 9
Db 6 RGDGGRGDS 14

RESULT 5

US-09-141-127-4

Sequence 4, Application US/09141127A

Patent No. 6083481

GENERAL INFORMATION:

APPLICANT: Dean, Richard T.

APPLICANT: Lister-James, John

TITLE OF INVENTION: THROMBUS IMAGING AGENTS

FILE REFERENCE: DITI 113.1USCI

CURRENT APPLICATION NUMBER: US/09/141,127A

CURRENT FILING DATE: 1998-08-27

EARLIER APPLICATION NUMBER: 08/335,832

EARLIER FILING DATE: 1995-01-05

EARLIER APPLICATION NUMBER: PCT/US93/04794

EARLIER FILING DATE: 1993-05-21

EARLIER APPLICATION NUMBER: 07/886,752

EARLIER FILING DATE: 1992-05-21

NUMBER OF SEQ ID NOS: 40

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 4

TYPE: PRT

LENGTH: 14

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: synthetic

OTHER INFORMATION: peptide

FEATURE:

NAME/KEY: MOD RES

LOCATION: (1)

OTHER INFORMATION: BLOCKED: acetamidomethyl

FEATURE:

NAME/KEY: MOD RES

LOCATION: (3)

OTHER INFORMATION: BLOCKED: acetamidomethyl

US-09-141-127-4

Query Match 40.8%; Score 29; DB 3; Length 14;
Best Local Similarity 66.7%; Pred. No. 2.4e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 RGDACXGDS 9
Db 6 RGDGGRGDS 14

RESULT 6

US-07-994-469A-19

Sequence 19, Application US/07994469A

Patent No. 5519119

GENERAL INFORMATION:

APPLICANT: Yamada, No. 5519119utoshi

APPLICANT: Kato, Masanari

APPLICANT: Miyata, Keizo

APPLICANT: Aoyama, Yoshiyuki

APPLICANT: Shikama, Hiroshi

TITLE OF INVENTION: Polypeptide

NUMBER OF SEQUENCES: 101

CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

P.C.

STREET: 1755 Jefferson Davis Highway, Fourth Floor
CITY: Arlington
STATE: Virginia
ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/994,469A
FILING DATE: 21-DEC-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5519119man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 72-085-0 FWC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)413-3000
TELEFAX: (703)413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-994-469A-19

Query Match 36.6%; Score 26; DB 1; Length 14;
Best Local Similarity 58.3%; Pred. No. 6.7e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

QY 1 RGDACXGDSGPP 12
Db 3 RGD--RGDSRAP 12

RESULT 7

PCT-US91-08328-35

Sequence 35, Application PC/TUS9108328

GENERAL INFORMATION:

APPLICANT: Ruggeri, Zaverio M.

APPLICANT: Houghten, Richard A.

TITLE OF INVENTION: PEPTIDES THAT INHIBIT PLATELET BINDING

TITLE OF INVENTION: OF ADHESION MOLECULES

NUMBER OF SEQUENCES: 47

CORRESPONDENCE ADDRESS:

ADDRESSEE: Eugene Moroz, MORGAN & FINNEGAN

STREET: 345 Park Avenue

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10154

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US91/08328

FILING DATE: 19911107

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/610,363

FILING DATE: 07-NOV-1990

ATTORNEY/AGENT INFORMATION:

NAME: Moroz, Eugene

REGISTRATION NUMBER: 25,237

REFERENCE/DOCKET NUMBER: 1198 4079PC

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)751-6849

TELEFAX: (212)751-6849

```
TELEX: 421792
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Disulfide-bond
; LOCATION: 1..>14
; OTHER INFORMATION: /note= "Sequence linked by
; OTHER INFORMATION: Interchain disulfide bond at Cys residue with Cys
; OTHER INFORMATION: residue on Arg-Ser-Arg-Gly-Asp-Val-Cys sequence"
; PUBLICATION INFORMATION:
; DOCUMENT NUMBER: US 4,683,291
; FILING DATE: 28-OCT-1985
; PUBLICATION DATE: 28-JUL-1987
; PUBLICATION INFORMATION:
; DOCUMENT NUMBER: US B1 4,683,291
; FILING DATE: 28-OCT-1985
; PUBLICATION DATE: 03-JUL-1990
PCT-US91-08328-35

Query Match 36.6%; Score 26; DB 5; Length 14;
Best Local Similarity 80.0%; Pred. No. 6.7e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RGDAC 5
Db 10 RGDVC 14

RESULT 8
PCT-US91-08328-36
; Sequence 36, Application PC/TUS9108328
; GENERAL INFORMATION:
; APPLICANT: Ruggeri, Zaverio M.
; TITLE OF INVENTION: PEPTIDES THAT INHIBIT PLATELET BINDING
; TITLE OF INVENTION: OF ADHESION MOLECULES
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eugene Moroz, MORGAN & FINNEGAN
; STREET: 345 Park Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: PCT/US91/08328
; FILING DATE: 19911107
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/610,363
; FILING DATE: 07-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Moroz, Eugene
; REGISTRATION NUMBER: 25,237
; REFERENCE/DOCKET NUMBER: 1198 4079PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)758-4800
; TELEFAX: (212)751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
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TELEX: AMINO ACID
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Disulfide-bond
; LOCATION: 1..>14
; OTHER INFORMATION: /note= "Sequence linked by
; OTHER INFORMATION: Interchain disulfide bond at Cys residue with Cys
; OTHER INFORMATION: residue on Arg-Gly-Arg-Gly-Asp-Val-Cys"
; PUBLICATION INFORMATION:
; DOCUMENT NUMBER: US 4,683,291
; FILING DATE: 28-OCT-1985
; PUBLICATION DATE: 28-JUL-1987
; PUBLICATION INFORMATION:
; DOCUMENT NUMBER: US B1 4,683,291
; FILING DATE: 28-OCT-1985
; PUBLICATION DATE: 03-JUL-1990
PCT-US91-08328-36

Query Match 36.6%; Score 26; DB 5; Length 14;
Best Local Similarity 80.0%; Pred. No. 6.7e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RGDAC 5
Db 10 RGDVC 14

RESULT 9
PCT-US91-08328-37
; Sequence 37, Application PC/TUS9108328
; GENERAL INFORMATION:
; APPLICANT: Ruggeri, Zaverio M.
; TITLE OF INVENTION: PEPTIDES THAT INHIBIT PLATELET BINDING
; TITLE OF INVENTION: OF ADHESION MOLECULES
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eugene Moroz, MORGAN & FINNEGAN
; STREET: 345 Park Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: PCT/US91/08328
; FILING DATE: 19911107
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/610,363
; FILING DATE: 07-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Moroz, Eugene
; REGISTRATION NUMBER: 25,237
; REFERENCE/DOCKET NUMBER: 1198 4079PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)758-4800
; TELEFAX: (212)751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
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ANTI-SENSE: NO
FEATURE:
NAME/KEY: Disulfide-bond
LOCATION: 1...>14
OTHER INFORMATION: /note= "Sequence linked by
OTHER INFORMATION: interchain disulfide bond at Cys residue with Cys
OTHER INFORMATION: residue on Arg8-Ala-Arg-Gly-Asp-Val-Cys sequence"
PUBLICATION INFORMATION:
DOCUMENT NUMBER: US 4,683,291
FILING DATE: 28-OCT-1985
PUBLICATION DATE: 28-JUL-1987
DOCUMENT NUMBER: US B1 4,683,291
PUBLICATION INFORMATION:
DOCUMENT NUMBER: US B1 4,683,291
FILING DATE: 28-OCT-1985
PUBLICATION DATE: 03-JUL-1990
PCT-US91-08328-37

Query Match 36.6%; Score 26; DB 5; Length 14;

Best Local Similarity 80.0%; Pred. No. 6.7e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RGDAC 5
Db 10 RGDVC 14

RESULT 10

PCT-US91-08328-38

Sequence 38, Application PC/TU99108328
GENERAL INFORMATION:
APPLICANT: Ruggeri, Zaverio M.
APPLICANT: Houghten, Richard A.
TITLE OF INVENTION: PEPTIDES THAT INHIBIT PLATELET BINDING
TITLE OF INVENTION: OF ADHESION MOLECULES
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:

ADDRESSEE: Eugene Moroz, MORGAN & FINNEGAN
STREET: 345 Park Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10154

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/08328
FILING DATE: 19911107

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/610,363

FILING DATE: 07-NOV-1990

ATTORNEY/AGENT INFORMATION:

NAME: Moroz, Eugene

REGISTRATION NUMBER: 25,237

REFERENCE/DOCKET NUMBER: 1198 4079PC

TELEPHONE: (212)758-4800

TELEFAX: (212)751-6849

TELEX: 421792

INFORMATION FOR SEQ ID NO: 38:

SEQUENCE CHARACTERISTICS:

LENGTH: 14 amino acids

TYPE: AMINO ACID

TOPOLOGY: unknown

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

ANTI-SENSE: NO

FEATURE:

NAME/KEY: Disulfide-bond

LOCATION: 1...>14

OTHER INFORMATION: /note= "Sequence linked by
OTHER INFORMATION: interchain bond at Cys residue with Cys residue on
PUBLICATION INFORMATION: Arg8-Leu-Arg-Gly-Asp-Val-Cys sequence"
DOCUMENT NUMBER: US 4,683,291
FILING DATE: 28-OCT-1985
PUBLICATION DATE: 28-JUL-1987
PUBLICATION INFORMATION:
DOCUMENT NUMBER: US B1 4,683,291
FILING DATE: 28-OCT-1985
PUBLICATION DATE: 03-JUL-1990
PCT-US91-08328-38

Query Match 36.6%; Score 26; DB 5; Length 14;

Best Local Similarity 80.0%; Pred. No. 6.7e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RGDAC 5
Db 10 RGDVC 14

RESULT 11

US-08-441-507-43

Sequence 43, Application US/08441507

Patent No. 6214358

GENERAL INFORMATION:

APPLICANT: Singh, Mohan Bir;

APPLICANT: Smith, Penelope; and

APPLICANT: Knox, Robert Bruce

TITLE OF INVENTION: Protein Allergens of the Species Cynodon

TITLE OF INVENTION: Dactylon

NUMBER OF SEQUENCES: 52

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD LLP

STREET: 28 State Street

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/441,507

FILING DATE: 15-May-1995

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/969,875

FILING DATE: 30-October-1992

ATTORNEY/AGENT INFORMATION:

NAME: Mandragouras, Amy E.

REGISTRATION NUMBER: 36,207

REFERENCE/DOCKET NUMBER: IMI-049DV

TELEPHONE: (617) 227-7400

TELEFAX: (617) 742-4214

INFORMATION FOR SEQ ID NO: 43:

SEQUENCE CHARACTERISTICS:

LENGTH: 14 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

FRAGMENT TYPE: internal

FEATURE:

NAME/KEY: Modified-site

LOCATION: 9

OTHER INFORMATION: /note= "Xaa is an unknown amino acid"

US-08-441-507-43

Query Match

35.2%; Score 25; DB 3; Length 14;

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Best Local Similarity 62.5%; Pred. No. 9.4e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 7 GDSGGPXV 14
Db 3 GDXPGPXI 10

RESULT 12
US-08-441-507-49
; Sequence 49, Application US/08441507
; Patent No. 621358
; GENERAL INFORMATION:
; APPLICANT: Singh, Mohan Bir;
; APPLICANT: Smith, Penelope; and
; APPLICANT: Knox, Robert Bruce
; TITLE OF INVENTION: Protein Allergens of the Species Cynodon
; TITLE OF INVENTION: Dactylon
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/441,507
; FILING DATE: 15-May-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/969,875
; FILING DATE: 30-October-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION/DOCKET NUMBER: 36,207
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 9
; OTHER INFORMATION: /note= "Xaa is an unknown amino acid"
US-08-441-507-49

Query Match 35.2%; Score 25; DB 3; Length 14;
Best Local Similarity 62.5%; Pred. No. 9.4e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 7 GDSGGPXV 14
Db 3 GDXPGPXI 10

RESULT 13
US-07-969-875A-43
; Sequence 43, Application US/07969875A
; Patent No. 6441157
; GENERAL INFORMATION:
; APPLICANT: Singh, Mohan Bir;

```

```

; APPLICANT: Smith, Penelope; and
; APPLICANT: Knox, Robert Bruce
; TITLE OF INVENTION: Protein Allergens of the Species
; TITLE OF INVENTION: Cynodon Dactylon
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunologic Pharmaceutical Corporation
; STREET: 610 Lincoln Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/969,875A
; FILING DATE: 30-October-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Vanstone, Darlene A.;
; REGISTRATION NUMBER: 35,279
; REFERENCE/DOCKET NUMBER: 041.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 466-6000
; TELEFAX: (617) 466-6010
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 9
; OTHER INFORMATION: /note= "Xaa is an unknown amino acid"
US-07-969-875A-43

Query Match 35.2%; Score 25; DB 4; Length 14;
Best Local Similarity 62.5%; Pred. No. 9.4e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 7 GDSGGPXV 14
Db 3 GDXPGPXI 10

RESULT 14
US-08-487-431-2
; Sequence 2, Application US/08487431
; Patent No. 5844090
; GENERAL INFORMATION:
; APPLICANT: Anderson, David C.
; APPLICANT: Mathews, Antony J.
; APPLICANT: Trimble, Stephen P.
; APPLICANT: Anthony-Cahill, Spencer
; TITLE OF INVENTION: Modified Hemoglobin-like Compounds
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Somatogen, Inc.
; STREET: 2545 Central Avenue, Suite FDI
; CITY: Boulder
; STATE: Colorado
; ZIP: 80301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: System 7.5
; SOFTWARE: Microsoft Word 5.0a
; CURRENT APPLICATION DATA:

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APPLICATION NUMBER: US/08/487,431
FILING DATE: June 7, 1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/240,712
FILING DATE: NO. 584090ember 6, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Theresa A.
REGISTRATION NUMBER: 32,547
REFERENCE/DOCKET NUMBER: 61
ATTORNEY/AGENT INFORMATION:
NAME: Ramsey R. Stewart
REGISTRATION NUMBER: 38,322
REFERENCE/DOCKET NUMBER: 61
TELECOMMUNICATION INFORMATION:
TELEPHONE: 303-541-3356
TELEFAX: 303-444-3013
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 14
TYPE: amino acid
TOPOLOGY: unknown to applicant
MOLECULE TYPE: peptide
HYPOTHETICAL: no
US-08-487-431-2

Query Match 33.8%; Score 24; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 1.3e+03;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 GDACXGDSGG 11
Db 2 GSGSGSGGG 11

RESULT 15
US-08-973-629-2
Sequence 2, Application US/08973629A
Patent No. 6150506
GENERAL INFORMATION:
APPLICANT: Trimble, Stephen
APPLICANT: Mathews, Anthony
APPLICANT: Kerwin, Bruce
APPLICANT: Marquardt, David
APPLICANT: Anthony-Cahill, Spencer
APPLICANT: Epp, Janice
APPLICANT: Madril, Dominic
APPLICANT: Anderson, David
TITLE OF INVENTION: MODIFIED HEMOGLOBIN-LIKE COMPOUNDS AND METHODS OF
FILE REFERENCE: BXTB 1928
CURRENT APPLICATION NUMBER: US/08/973,629A
CURRENT FILING DATE: 1998-08-24
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 14
TYPE: PPT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence :Peptide linker
Patent No. 6150506
OTHER INFORMATION: to couple dialpha domains
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Peptide linker
OTHER INFORMATION: to couple dialpha domains
US-08-973-629-2

Query Match 33.8%; Score 24; DB 3; Length 14;
Best Local Similarity 50.0%; Pred. No. 1.3e+03;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 GDACXGDSGG 11

Db 2 GSGSGSGGG 11
Search completed: February 26, 2004, 09:43:05
Job time : 25 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: February 26, 2004, 09:46:33 ; Search time 21 Seconds

(without alignments)
114,514 Million cell updates/sec

Title: US-09-909-348-5

Perfect score: 141

Sequence: 1 AGTRYKPDGKRGDACEGSGPFFV 25

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 248

Minimum DB seq length: 25

Maximum DB seq length: 25

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 78:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	19.9	25	2 S13996	hypothetical prote
2	26	18.4	25	2 I51565	protein-tyrosine k
3	26	18.4	25	2 A34179	neuromedin U - com
4	26	18.4	25	2 D42397	KU antigen 84K pro
5	25	17.7	25	2 S07770	histone H2B.1, spe
6	25	17.7	25	2 A46543	neuromedin U - chi
7	23	16.3	25	2 A30590	cytolytic enteroto
8	23	16.3	25	2 T01689	ATPase-beta chain
9	22	15.6	25	2 A60807	heat shock protein
10	22	15.6	25	2 T09385	rev protein - huma
11	22	15.6	25	2 S55765	interferon-inducib
12	22	15.6	25	2 B85928	hypothetical prote
13	21.5	15.2	25	2 I56978	collagen alpha 2(X
14	21.5	15.2	25	2 A60741	insulin-like growt
15	21	14.9	25	2 D26889	T-cell receptor be
16	21	14.9	25	2 S28993	antifungal protein
17	21	14.9	25	2 E41506	homeotic protein M
18	21	14.9	25	2 S22234	vitronectin - chic
19	20.5	14.5	25	2 B86074	hypothetical prote
20	20	14.2	25	2 A20596	venom kallikrein (
21	20	14.2	25	2 B20596	venom kallikrein (
22	20	14.2	25	2 JH0701	omega-conotoxin MV
23	20	14.2	25	2 JH0700	omega-conotoxin MV
24	20	14.2	25	2 PH1716	Ig heavy chain V r
25	20	14.2	25	2 PH1910	T-cell receptor al
26	20	14.2	25	2 S03409	tubulin alpha chai
27	20	14.2	25	2 S10797	hypothetical prote
28	20	14.2	25	2 S17683	hypothetical prote
29	20	14.2	25	2 PH1907	T-cell receptor al

30 20 14.2 25 2 S22228
31 20 14.2 25 2 S21768
32 20 14.2 25 2 S74094
33 20 14.2 25 2 S22227
34 20 14.2 25 2 PX0044
35 19.5 13.8 25 2 S21515
36 19 13.5 25 1 2JBPG4
37 19 13.5 25 2 A35545
38 19 13.5 25 2 B44524
39 19 13.5 25 2 S07250
40 19 13.5 25 2 A61148
41 19 13.5 25 2 S74108
42 19 13.5 25 2 JN0309
43 19 13.5 25 2 S44201
44 19 13.5 25 2 S47190
45 19 13.5 25 2 PC4445

vitronectin - dog
vitronectin - rabb
fibulin 1 variant
vitronectin - guin
6-phosphofructokin
finP protein - Esc
gene J protein - p
T-kininogenase (EC
pregnancy-specific
hypothetical prote
cyanidase (EC 3.5.
hemolysin A - vibr
insulin-binding pr
HLA-DRB1 exon2 pro
T-cell receptor J-
L-ascorbate peroxi

ALIGNMENTS

RESULT 1

S13996
hypothetical protein - phase TW19 (fragment)

C/Species: phage TW19

C/Date: 18-Feb-1994 #sequence_revision 24-Apr-1998 #text_change 24-Apr-1998

C/Accession: S13996

R/Inokuchi, Y.; Hirashima, A.; Watanabe, I.

J. Mol. Biol. 158, 711-730, 1982

A/Title: Comparison of the nucleotide sequences at the 3'-terminal region of RNAs from R

A/Reference number: S07250; MUID:83010313; PMID:7120417

A/Accession: S13996

A/Status: translation not shown

A/Molecule type: genomic RNA

A/Residues: 1-25 <INO>

A/Cross-references: EMBL:J02520; NID:g216180

Query Match 19.9%; Score 28; DB 2; Length 25;

Best Local Similarity 50.0%; Pred. No. 1.9e+03;

Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 9 EGRKGDAEG 18

Db 7 ERKTPSCEG 16

RESULT 2

I51565

protein-tyrosine kinase (EC 2.7.1.112) src - African clawed frog (fragment)

C/Species: Xenopus laevis (African clawed frog)

C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 04-Mar-2000

C/Accession: I51565

R/Steale, R.E.

Nucleic Acids Res. 13, 1747-1761, 1985

A/Title: Two divergent cellular src genes are expressed in Xenopus laevis.

A/Reference number: I51563; MUID:85215578; PMID:2987836

A/Accession: I51565

A/Status: preliminary; translated from GB/EMBL/DDBJ

A/Molecule type: mRNA

A/Residues: 1-25 <STB>

A/Cross-references: GS:M30859; NID:g214811; PID:AAA49964.1; PID:g214814

C/Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 f

C/Keywords: ATP; blocked amino end; lipoprotein; myristylation; phosphorylation; phosphotransferase; tyrc

F.2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted

Query Match 18.4%; Score 26; DB 2; Length 25;

Best Local Similarity 62.5%; Pred. No. 3.5e+03;

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TRYKPDG 10

Db 4 TKSKPREG 11

RESULT 3

A34179
neuromedin U - common frog
C:Species: Rana temporaria (common frog)
C>Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 18-Jun-1993
C:Accession: A34179
R:Domian, J.; Yiangou, Y.; Spokes, R.A.; Aitken, A.; Parmar, K.B.; Chrysanthou, B.J.; Bld
J. Biol. Chem. 264, 20881-20885, 1989
A:Title: The distribution, purification, and pharmacological action of an amphibian neu
A:Reference number: A34179; MUID:90078173; PMID:2592357
A:Accession: A34179
A:Molecule type: protein
A:Residues: 1-25 <DOM>

Query Match 18.4%; Score 26; DB 2; Length 25;
Best Local Similarity 62.5%; Pred. No. 3.5e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 KPDEGKRG 13

DB 2 KPDEELQG 9

RESULT 4

D42397
Ku antigen 84K protein (fraction 15) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 11-Apr-1995
C:Accession: D42397
R:Wedrychoweki, A.; Henzel, W.; Huston, L.; Paslidis, N.; Ellerson, D.; McRae, M.; Seong
J. Biol. Chem. 267, 4533-4540, 1992
A:Title: Identification of proteins binding to interferon-inducible transcriptional enh
A:Reference number: A42397; MUID:92165807; PMID:1537839
A:Accession: D42397
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-25 <WED>
A:Experimental source: K562 cells
A:Note: sequence extracted from NCBI backbone (NCBIP:85285)

Query Match 18.4%; Score 26; DB 2; Length 25;
Best Local Similarity 43.8%; Pred. No. 3.5e+03;
Matches 7; Conservative 2; Mismatches 5; Indels 2; Gaps 1;

QY 9 EGKRGD--ACRGDSGG 22

DB 1 DGPSGDTAAVFEEGG 16

RESULT 5

S07770
histone H2B.1, sperm - sea urchin (Echinus esculentus) (fragment)
C:Species: Echinus esculentus
C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 23-Feb-1997
C:Accession: S07770
R:Hall, C.S.; Thomas, J.O.
Eur. J. Biochem. 187, 145-153, 1990
A:Title: Core histone-DNA interactions in sea urchin sperm chromatin. The N-terminal tail
A:Reference number: S07769; MUID:90126812; PMID:2298202
A:Accession: S07770
A:Molecule type: protein
A:Residues: 1-25 <HIL>
C:Superfamily: histone H2B
C:Keywords: chromosomal protein; DNA binding; nucleosome core; nucleus

Query Match 17.7%; Score 25; DB 2; Length 25;
Best Local Similarity 36.4%; Pred. No. 4.8e+03;
Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 3 TRYKPEGKRG 13

DB 12 TKRSFQKGKG 22

RESULT 6

A48543
neuromedin U - chicken
C:Species: Gallus gallus (chicken)
C>Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 23-Mar-1995
C:Accession: A48543
R:Domian, J.; Benito-Orfila, M.A.; Nandha, K.A.; Aitken, A.; Bloom, S.R.
Regul. Pept. 41, 1-8, 1992
A:Title: The purification and sequence analysis of an avian neuromedin U.
A:Reference number: A48543; MUID:93087774; PMID:1455013
A:Accession: A48543
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-25 <DOM>
A:Experimental source: small intestine
A:Note: sequence extracted from NCBI Backbone (NCBIP:120483)

Query Match 17.7%; Score 25; DB 2; Length 25;
Best Local Similarity 55.6%; Pred. No. 4.8e+03;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 YKPEGKRG 13

DB 1 YKVEDDLQG 9

RESULT 7

A30590
Cytolytic enterotoxin - Aeromonas hydrophila (fragment)
C:Species: Aeromonas hydrophila
C>Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 11-Jan-2000
C:Accession: A30590
R:Rose, J.M.; Houston, C.W.; Coppenhaver, D.H.; Dixon, J.D.; Kurosky, A.
Infect. Immun. 57, 1165-1169, 1989
A:Title: Purification and chemical characterization of a cholera toxin-cross-reactive c
A:Reference number: A30590; MUID:89173315; PMID:2925244
A:Accession: A30590
A:Molecule type: protein
A:Residues: 1-25 <ROS>
C:Superfamily: aerolysin

Query Match 16.3%; Score 23; DB 2; Length 25;
Best Local Similarity 50.0%; Pred. No. 9e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GTRYKP 7

DB 20 GDKYRP 25

RESULT 8

T01689
ATPase-beta chain - maize chloroplast (fragment)
C:Species: chloroplast Zea mays (maize)
C>Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 29-Oct-1999
C:Accession: T01689
R:Bradley, D.; Gatenby, A.A.
EMBO J. 4, 3641-3648, 1985
A:Title: Mutational analysis of the maize chloroplast ATPase-beta subunit gene promoter
system.
A:Reference number: Z14396; MUID:86136006; PMID:3004965
A:Accession: T01689
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-25 <BRA>
A:Cross-references: EMBL:X03396; NID:gi2404; PIDN:CAA27131.1; PID:gi2405
C:Genetics:
A:Genome: chloroplast
C:Keywords: chloroplast

Query Match 16.3%; Score 23; DB 2; Length 25;

A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-25 <TUR>

Query Match 15.6%; Score 22; DB 2; Length 25;
Best Local Similarity 41.7%; Pred. No. 1.2e+04;
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 AGTRYKPEQKR 12
|||
8 AGENAGKDAGKK 19

RESULT 12
B85928
C:Species: Escherichia coli
C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C:Accession: B85928
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: B85928
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-25 <STO>
A:Cross-references: GR:AB005174; NID:G12517242; PIDN:AA057886.1; GSPDB:GN00145; UWPG:Z40
A:Experimental source: strain O157:H7, Substrain EDL933
C:Genetics:
A:Gene: Z4088

Query Match 15.6%; Score 22; DB 2; Length 25;
Best Local Similarity 55.6%; Pred. No. 1.2e+04;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 YKPDSEKKG 13
|||
DB 9 YFEHGLRG 17

RESULT 13
I56978
C:Species: Bos primigenius taurus (cattle)
C>Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 05-Dec-1998
C:Accession: I56978
R:Wu, J.J.; Eyre, D.R.
J. Biol. Chem. 270, 18665-18670, 1995
A:Title: Structural analysis of cross-linking domains in cartilage type XI collagen. Ins
A:Reference number: A56978; MUID:95370194; PMID:7642541
A:Accession: I56978
A>Status: preliminary
A:Molecule type: Protein
A:Residues: 1-25 <WUA>
A>Note: the residue designated 'X' is modified lysine cross-linked to 1(II) Lys-3 in D56
C:Superfamily: collagen alpha 1(V) chain; fibrillar collagen carboxyl-terminal homology
C:Keywords: hydroxylysine; hydroxyproline
F;6/Modified site: 5-hydroxylysine (Lys) #status experimental
F;12,21/Modified site: 4-hydroxyproline (Pro) #status experimental

Query Match 15.2%; Score 21.5; DB 2; Length 25;
Best Local Similarity 41.7%; Pred. No. 1.4e+04;
Matches 5; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

QY 13 GD-ACEGDSGGP 23
|||
DB 1 GDTCAKGEXGHP 12

RESULT 14
A60741

insulin-like growth factor-binding protein He39L - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 30-Sep-1993
 C/Accession: A60741
 R/Forbes, B.; Ballard, F.J.; Wallace, J.C.
 J. Endocrinol. 126, 497-506, 1990
 A/Title: An insulin-like growth factor-binding protein purified from medium conditioned
 A/Reference number: A60741; MUID:91011238; PMID:1698907
 A/Accession: A60741
 A/Status: Preliminary
 A/Molecule type: protein
 A/Residues: 1-25 <FOR>

Query Match 15.2%; Score 21.5; DB 2; Length 25;
 Best Local Similarity 33.3%; Pred. No. 1.4e+04;
 Matches 7; Conservative 2; Mismatches 7; Indels 5; Gaps 1;

Qy 7 PDEGK-----GDACEGDSGG 22
 Db 5 PQGVQAGXPGXVEEDRGG 25

RESULT 15

D26889
 T-cell receptor beta chain V-J-C regions (52H10F11) - mouse (fragment)
 C/Species: Mus musculus (house mouse)
 C/Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 30-May-1997
 C/Accession: D26889
 R/Sherman, D.H.; Hochman, P.S.; Dick, R.; Tizard, R.; Ramachandran, K.L.; Flavell, R.A.;
 Mol. Cell. Biol. 7, 1865-1872, 1987
 A/Title: Molecular analysis of antigen recognition by insulin-specific T-cell hybridomas
 A/Reference number: A26889; MUID:87257888; PMID:2439899
 A/Accession: D26889
 A/Molecule type: mRNA
 A/Residues: 1-25 <SHE>
 A/Cross-references: GB:M16121
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: T-cell receptor

Query Match 14.9%; Score 21; DB 2; Length 25;
 Best Local Similarity 60.0%; Pred. No. 1.7e+04;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 17 EGDGG 21
 Db 7 DGDG 11

Search completed: February 26, 2004, 09:50:07
 Job time : 23 secs

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OM protein - protein search, using sw model

Run on: February 26, 2004, 09:43:07 ; Search time 11 Seconds
(without alignments)
118.341 Million cell updates/sec

Title: US-09-909-348-5

Perfect score: 141
Sequence: 1 AGTRYKPDGKRGDACEGSGGFV 25

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 103

Minimum DB seq length: 25
Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26	18.4	25	1 NEUU_RANTE	P20056 rana tempor
2	25	17.7	25	1 BT12_BOOMI	P83603 boophilus m
3	25	17.7	25	1 CYC4_VTBFI	P80891 vibrio fisc
4	25	17.7	25	1 H2B1_ECHES	P13281 echinus esc
5	25	17.7	25	1 NEUU_CHICK	P34963 gallus gall
6	23	16.3	25	1 B0TR_BOTJA	P22028 bothrops ja
7	21	14.9	25	1 CXOB_CONCT	P58918 conus catus
8	20	14.2	25	1 CXOB_CONMA	P05485 conus magus
9	20	14.2	25	1 K6P2_TRETH	P21778 thermus the
10	20	14.2	25	1 TBA_LERPE	P10489 leptomonas
11	19	13.5	25	1 HCY3_MAISO	P82304 maia squina
12	19	13.5	25	1 VGU_PIG	P34964 sus scrofa
13	19	13.5	25	1 MT_AGABI	P03652 bacterioph
14	18.5	13.1	25	1 MT_NEUCR	P04358 agaricus di
15	18.5	13.1	25	1 MT_NEUCR	P02807 neurospora
16	18	12.8	25	1 BT14_BOOMI	P83605 boophilus m
17	18	12.8	25	1 GBP_APAPA	P22800 apanteles k
18	18	12.8	25	1 LE01_BIOGL	P80742 biophalari
19	18	12.8	25	1 OM53_PORGI	P81363 porphyromon
20	18	12.8	25	1 Y194_ARCFU	O30045 archaeglob
21	17.5	12.4	25	1 FLAA_TREPH	P21983 treponema p
22	17	12.1	25	1 BGBP_PENVA	P81182 penaeus van
23	17	12.1	25	1 CP12_SOLTU	P24744 solanum tub
24	17	12.1	25	1 CX6A_CONQU	P58843 conus querc
25	16	11.3	25	1 AHPC_ACICA	P82954 acinetobact
26	16	11.3	25	1 AMP3_MELGA	P80393 melalegris g
27	16	11.3	25	1 COX1_PARVE	Q00502 paracoccila
28	16	11.3	25	1 GLMK_PREBR	P82850 prevotella
29	16	11.3	25	1 IPYR_PSEAN	P80898 pseudanabae
30	16	11.3	25	1 LYC_ASTRU	P37715 asterias ru
31	16	11.3	25	1 SCRK_LACLA	Q09124 lactococcus
32	15	10.6	25	1 ANDT_ANDAU	P56684 androctonus
33	15	10.6	25	1 ATPD_MICLU	P80285 micrococcus

34	15	10.6	25	1 COXO_ONCMY	P80334 oncorhynch
35	15	10.6	25	1 G3P2_JACOR	P80447 iaculus ori
36	15	10.6	25	1 H1L_WHEAT	P15871 triticum ae
37	15	10.6	25	1 NEUU_CANFA	P34962 canis famil
38	15	10.6	25	1 RIP_FLAVE	P83324 flammulina
39	15	10.6	25	1 SODC_PAROL	P83129 paralichthy
40	14	9.9	25	1 ATPY_SOLTU	P80497 solanum tub
41	14	9.9	25	1 CHV1_PAGMA	P83545 pagrus majo
42	14	9.9	25	1 CHV2_PAGMA	P83546 pagrus majo
43	14	9.9	25	1 COX5_NEUCR	Q01359 neurospora
44	14	9.9	25	1 HCY2_CARMA	P83177 carcinus ma
45	14	9.9	25	1 IAA_SECCE	P83048 secale cere

ALIGNMENTS

RESULT 1
NEUU_RANTE
ID NEUU_RANTE STANDARD; PRT; 25 AA.
AC P20056;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuromedin U-25 (NMU-25).
OS Rana temporaria (European common frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8407;
RN [1]
RP SEQUENCE.
RC TISSUE=Intestine; PubMed=2592357;
RX MEDLINE=90078173; PubMed=2592357;
RA Domin J., Yanguo Y.G., Spokes R.A., Aitken A., Parmar K.B.,
RA Chrysanthou B.J., Bloom S.R.;
RT "The distribution, purification, and pharmacological action of an
RT amphibian neuromedin U";
RL J. Biol. Chem. 264:20881-20885(1989).
CC -!- FUNCTION: Stimulates uterine smooth muscle contraction and causes
CC selective vasoconstriction.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the NMU family.
DR PIR; A34179; A34179.
DR InterPro; IPR008199; NMU.
DR Pfam; PF02070; NMU; 1.
DR SMART; SM00084; NMU; 1.
DR PROSITE; PS00967; NMU; 1.
DR KW Amidation; Hormone.
FT MOD RES 25
SQ SEQUENCE 25 AA; 2832 MW; 6A01D89F6DA06FD4 CRC64;
Query Match 18.4%; Score 26; DB 1; Length 25;
Best Local Similarity 62.5%; Pred. No. 1.5e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
OY 6 KPDEGKRG 13
DB 2 KPDEELQG 9
RESULT 2
BT12_BOOMI
ID BT12_BOOMI STANDARD; PRT; 25 AA.
AC P83603;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Kunitz-type serine protease inhibitor BmT1-2 (Fragment).
OS Boophilus microplus (Cattle tick).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Parasitiformes; Ixodida; Ixodidae; Boophilus.
OX NCBI_TaxID=6941;
RN [1]

RP SEQUENCE, AND FUNCTION.

RC TISSUE=Larva;
 RA Sasaki S.D., Hirata I.Y., Tanaka A.S.;
 RT "Molecular studies of serine protease inhibitors from cattle tick
 Bophilus microplus (larvae).";
 RL Submitted (JUN-2003) to Swiss-Prot.
 CC -!- FUNCTION: Inhibits trypsin, human plasma kallikrein and human
 CC neutrophil elastase.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 DR InterPro; IPR002223; Kunitz BPTI.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; PARTIAL.
 DR PROSITE; PS02079; BPTI_KUNITZ_2; PARTIAL.
 KW Serine protease inhibitor.
 FT ACT SITE 17 18 REACTIVE BOND (BY SIMILARITY).
 FT NON TER 25 25
 SQ SEQUENCE 25 AA; 2691 MW; D8E538C2C2B20466 CRC64;

Query Match 17.7%; Score 25; DB 1; Length 25;
 Best Local Similarity 46.2%; Pred. No. 2.1e+03;
 Matches 6; Conservative 1; Mismatches 4; Indels 2; Gaps 1;

QY 13 GDACE--GDGGGP 23
 | | | | |
 Db 4 GPVCELPKEVGPP 16

RESULT 3

CYC4 VIBFI
 ID -CYC4 VIBFI STANDARD; PRT; 25 AA.

AC P80891;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Putative cytochrome C4 (C551) (fragment).
 OS Vibrio fischeri.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrionaceae; Vibrio.
 OX NCBI_TaxID=668;
 RN [1]
 RP SEQUENCE.

RC STRAIN=ATCC 33715 / Y-1;
 RX MEDLINE=97326008; PubMed=9183020;
 RA Petushkov V.N., Lee J.;
 RT "Purification and characterization of flavoproteins and cytochromes
 RT from the yellow bioluminescence marine bacterium Vibrio fischeri
 RT strain Y1.";
 RL Eur. J. Biochem. 245: 790-796 (1997).
 CC -!- FUNCTION: DIHEME, HIGH POTENTIAL CYTOCHROME C BELIEVED TO BE AN
 CC INTERMEDIATE ELECTRON DONOR TO TERMINAL OXIDATION SYSTEMS (BY
 CC SIMILARITY).

CC -!- SUBCELLULAR LOCATION: Periplasmic (By similarity).
 CC -!- PTM: Binds two 2 groups per molecule (By similarity).
 CC InterPro; IPR000345; Cytochrome BS.
 DR PROSITE; PS00190; CYTOCHROME_C7_1.
 KW Electron transport; Heme; Periplasmic.
 FT BINDING 14 14 HEME 1 (COVALENT) (BY SIMILARITY).
 FT BINDING 17 17 HEME 1 (COVALENT) (BY SIMILARITY).
 FT UNSURE 14 14
 FT UNSURE 17 17
 FT NON TER 25 25
 SQ SEQUENCE 25 AA; 2594 MW; CFB0D9A5933186C7 CRC64;

Query Match 17.7%; Score 25; DB 1; Length 25;
 Best Local Similarity 57.1%; Pred. No. 2.1e+03;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 15 ACEGDSG 21
 | | | | |
 Db 16 ACHQEG 22

RESULT 4

H2B1 ECHES

ID H2B1 ECHES STANDARD; PRT; 25 AA.
 AC P13281;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Histone H2B.1, sperm (fragment).
 OS Echinus esculentus (Sea urchin).
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
 OC Echinoidea; Euechinoidea; Echinacea; Echinoida; Echinidae; Echinus.
 OX NCBI_TaxID=7648;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=90126812; PubMed=2298202;
 RA Hill C.S., Thomas J.O.;
 RT "Core histone-DNA interactions in sea urchin sperm chromatin. The N-
 RT terminal tail of H2B interacts with linker DNA.";
 RL Eur. J. Biochem. 187:145-153 (1990).
 CC -!- SUBUNIT: The nucleosome is an octamer containing two molecules
 CC each of H2A, H2B, H3 and H4. The octamer wraps approximately 146
 CC bp of DNA.
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- SIMILARITY: Belongs to the histone H2B family.
 DR InterPro; IPR000558; Histone H2B.
 DR PROSITE; PS00357; HISTONE_H2B; PARTIAL.
 KW Nuclear protein; Chromosomal protein; Nucleosome core; DNA-binding;
 FT NON TER 25 25
 SQ SEQUENCE 25 AA; 2693 MW; 9842DD3D73A3A9EC CRC64;

Query Match 17.7%; Score 25; DB 1; Length 25;
 Best Local Similarity 36.4%; Pred. No. 2.1e+03;
 Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 3 TRYKPDGKRG 13
 | | | | |
 Db 12 TKRSPQKGKG 22

RESULT 5

NEUU_CHICK
 ID NEUU_CHICK STANDARD; PRT; 25 AA.

AC P34963;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Neuromedin U-25 (NMU-25) [Contains: Neuromedin U-9 (NMU-9)].
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=93087774; PubMed=1455013;
 RA Domin J., Benito-Orfila M.A., Nandha K.A., Aitken A., Bloom S.R.;
 RT "The purification and sequence analysis of an avian neuromedin U.";
 RL Regul. Pept. 41:1-8 (1992).
 RN [2]
 RP SEQUENCE OF 17-25.

RC TISSUE=Intestine;
 RX MEDLINE=92158816; PubMed=1788145;
 RA O'Harte F., Bockman C.S., Zeng W., Abel P.W., Harvey S., Conlon J.M.;
 RT "Primary structure and pharmacological activity of a nonapeptide
 RT related to neuromedin U isolated from chicken intestine.";
 RL Peptides 12:809-812 (1991).
 CC -!- FUNCTION: Stimulates uterine smooth muscle contraction and causes
 CC selective vasoconstriction.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the NMU family.
 DR InterPro; IPR008199; NMU.


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FT DISULFID 1 16
FT DISULFID 8 20
FT DISULFID 15 25
FT MOD RES 25 25
SQ SEQUENCE 25 AA; 2626 MW; 54B9CE5EFAA3734D CRC64;
  Query Match 14.2%; Score 20; DB 1; Length 25;
  Best Local Similarity 60.0%; Pred. No. 9.8e+03; Indels 0; Gaps 0;
  Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 14 DACEG 18
DB 14 DCCGTG 18
  RESULT 9
  K6P2 THETH STANDARD; PRT; 25 AA.
AC P21778;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE 6-phosphofructokinase isozyme 2 (EC 2.7.1.11) (Phosphofructokinase-2)
DE (PFK2) (Phosphohexokinase 2) (Fragment).
OS Thermus thermophilus.
OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
OC Thermus.
OX NCBI_TaxID=274;
RN [1]
RP SEQUENCE.
RC STRAIN=HB8 / ATCC 27634;
RX MEDLINE=91324297; PubMed=1830879;
RA Xu J., Oshima T., Yoshida M.;
RT "Phosphoenolpyruvate-insensitive phosphofructokinase isozyme from
RT Thermus thermophilus HB8.";
RL J. Biochem. 109:199-203(1991).
CC -!- CATALYTIC ACTIVITY: ATP + D-fructose 6-phosphate = ADP + D-
CC fructose 1,6-bisphosphate.
CC -!- ENZYME REGULATION: IN CONTRAST WITH PFK1 THIS ENZYME IS NOT
CC AFFECTED BY PHOSPHOENOLPYRUVATE.
CC -!- PATHWAY: Key control step of glycolysis.
CC -!- SUBUNIT: Homotetramer.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to the phosphofructokinase family.
DR HSP; P00512; 3PK.
DR HAMAP; MF_00339; -; 1.
DR InterPro; IPR000023; Ppfruckinase.
DR Pfam; PF00365; PFK, 1.
DR PROSITE; PS00433; PHOSPHOFRUCTOKINASE; PARTIAL.
KW Kinase; Transferase; Glycolysis; Multigene family.
FT NON TER 25 25
SQ SEQUENCE 25 AA; 2557 MW; E7AEC8D6110EBA46 CRC64;
  Query Match 14.2%; Score 20; DB 1; Length 25;
  Best Local Similarity 80.0%; Pred. No. 9.8e+03; Indels 0; Gaps 0;
  Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 18 GDSGG 22
DB 11 GDSPG 15
  RESULT 10
  TBA LEFSE STANDARD; PRT; 25 AA.
AC P10489;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Tubulin alpha chain (Fragment).
OS Leptomonas seymouri.
OC Eukaryota; Eulenczoa; Kinetoplastida; Trypanosomatidae; Leptomonas.
OX NCBI_TaxID=5684;
  RESULT 11
  HCV3 MAISO STANDARD; PRT; 25 AA.
ID HCV3 MAISO
AC P82304;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hemocyanin subunit 3 (Fragment).
OS Maia squinado (Spiny spider crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Majoidae; Majidae; Maia.
OX NCBI_TaxID=99391;
RN [1]
RP SEQUENCE.
RX MEDLINE=99259579; PubMed=10327595;
RA Stoeva S., Dolashka P., Hristova R., Genov N., Voelter W.;
RT "Subunit composition and N-terminal analysis of arthropod
RT hemocyanins.";
RL Comp Biochem. Physiol. 122B:69-75(1999).
CC -!- FUNCTION: Hemocyanins are copper-containing oxygen carriers
CC occurring freely dissolved in the hemolymph of many mollusks and
CC arthropods.
CC -!- SUBCELLULAR LOCATION: Extracellular.
CC -!- TISSUE SPECIFICITY: Hemolymph.
CC -!- SIMILARITY: Belongs to the tyrosinase family. Hemocyanin
CC subfamily.
DR InterPro; IPR000896; Hemocyanin.
DR InterPro; IPR002227; Tyrosinase.
DR PROSITE; PS00209; HEMOCYANIN 1; PARTIAL.
DR PROSITE; PS00210; HEMOCYANIN 2; PARTIAL.
DR PROSITE; PS00497; TYROSINASE 1; PARTIAL.
DR PROSITE; PS00498; TYROSINASE 2; PARTIAL.
DR PROSITE; PS00499; TYROSINASE 2; PARTIAL.
KW Transport; Oxygen transport; Copper; Hemolymph.
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FT NON_TER 25 25
SQ SEQUENCE 25 AA; 2689 MW; 5DCB84PFF9A45F67 CRC64;

Query Match 13.5%; Score 19; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 GGP 23
DB 1 GGP 3

RESULT 12
NEU_PIG
ID NEU_PIG STANDARD; PRT; 25 AA.
AC P34564;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuromedin U-25 (NMU-25) [Contains: Neuromedin U-8 (NMU-8)].
GN NMU.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RV [1]
RP SEQUENCE.
RC TISSUE=Spinal cord; PubMed=3839674;
RX MEDLINE=85279502; PubMed=3839674;
RA "Mitsunori N., Kangawa K., Matsuo H.;
RT "Neuromedin U-8 and U-25: novel uterus stimulating and hypertensive
RT peptides identified in porcine spinal cord.";
RL Biochem. Biophys. Res. Commun. 130:1078-1085(1985).
CC -!- FUNCTION: Stimulates uterine smooth muscle contraction and causes
CC selective vasoconstriction.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the NMU family.
DR InterPro: IPR008199; NMU.
DR Pfam: PF02070; NMU; 1.
DR SMART: SM00084; NMU; 1.
DR PROSITE: PS00967; NMU; 1.
KW Amidation; Hormone; Cleavage on pair of basic residues.
FT PEPTIDE 1 25 NEUROMEDIN U-25.
FT PEPTIDE 18 25 NEUROMEDIN U-8.
FT MOD_RES 25 25 AMIDATION.
SQ SEQUENCE 25 AA; 3144 MW; 46A065C120F193B9 CRC64;

Query Match 13.5%; Score 19; DB 1; Length 25;
Best Local Similarity 44.4%; Pred. No. 1.3e+04;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 5 YKPEGKKG 13
DB 1 FKVDEFGQ 9

RESULT 13
VGJ_BPG4
ID VGJ_BPG4 STANDARD; PRT; 25 AA.
AC P03652;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Small core protein (J protein).
GN J.
OS Bacteriophage G4.
OC Viruses; ssDNA viruses; Microviridae; Microvirus.
OX NCBI_TaxID=10843;
RV [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=79053264; PubMed=714153;
RA Godson G.N., Barrell B.G., Staden R., Fiddes J.C.;
RT "Nucleotide sequence of bacteriophage G4 DNA.";
```

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RL Nature 276:236-247(1978).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
RX MEDLINE=96217890; PubMed=8642594;
RA McKenna R., Bowman B.R., Irag L.L., Rossmann M.G., Fane B.A.;
RT "Atomic structure of the degraded procapsid particle of the
RT bacteriophage G4: induced structural changes in the presence of
RT calcium ions and functional implications.";
RL J. Mol. Biol. 256:736-750(1996).
CC -!- FUNCTION: The J protein is associated with the DNA and is situated
CC in an interior cleft of the F protein.
CC -!- SUBUNIT: The virion is composed of 60 copies each of the F, G, and
CC J proteins, and 12 copies of the H protein.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: V00657; CAA24018.1; -.
DR PIR: A04259; ZJBPG4.
DR PDB: 1GFF; 03-APR-96.
DR InterPro: IPR006815; Microvir_J.
DR Pfam: PF04726; Microvir_J; 1.
KW Coat protein; DNA-binding; 3D-structure.
SQ SEQUENCE 25 AA; 2815 MW; 87B7A8DFFD6D033 CRC64;

Query Match 13.5%; Score 19; DB 1; Length 25;
Best Local Similarity 75.0%; Pred. No. 1.3e+04;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTRY 5
DB 22 GTQY 25

RESULT 14
MT_AGABI
ID MT_AGABI STANDARD; PRT; 25 AA.
AC P04358;
DT 20-MAR-1984 (Rel. 04, Created)
DT 20-MAR-1984 (Rel. 04, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Metallothionein (MT).
OS Agaricus bisporus (Common mushroom).
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Agaricales; Agaricaceae; Agaricus.
OX NCBI_TaxID=5341;
RV [1]
RP SEQUENCE.
RC STRAIN=A-32; TISSUE=Mycelium;
RA Muenger K., Lerch K.;
RT "Copper metallothionein from the fungus Agaricus bisporus: chemical
RT and spectroscopic properties.";
RL Biochemistry 24:6751-6756(1985).
CC -!- FUNCTION: The metallothioneins are involved in the cellular
CC sequestration of toxic metal ions. Binds six copper (cuprous)
CC ions.
CC -!- MISCELLANEOUS: The absorption, luminescent, and stereoptical
CC properties of the copper MT are attributed to the metal-thiolate
CC complex because they are not present in the apoprotein.
CC -!- SIMILARITY: BELONGS TO THE METALLOTHIONEIN SUPERFAMILY; FAMILY 8.
DR PIR: A03286; SNMR.
KW Metal-binding; Metal-thiolate cluster; Copper.
SQ SEQUENCE 25 AA; 2233 MW; 33AB70F21023CFF7 CRC64;

Query Match 13.1%; Score 18.5; DB 1; Length 25;
Best Local Similarity 55.6%; Pred. No. 1.5e+04;
Matches 5; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
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OM protein - protein search, using sw model

Run on: February 26, 2004, 09:46:13 ; Search time 38 Seconds
(without alignments)
207.578 Million cell updates/sec

Title: US-09-909-348-5

Perfect score: 141
Sequence: 1 ACRYKPDGKRGDAACGDSGPFV 25

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 841

Minimum DB seq length: 25
Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL.25: *
1: sp_archaea: *
2: sp_bacteria: *
3: sp_fungi: *
4: sp_human: *
5: sp_invertebrate: *
6: sp_mammal: *
7: sp_mhc: *
8: sp_organelle: *
9: sp_phage: *
10: sp_plant: *
11: sp_podent: *
12: sp_virus: *
13: sp_vertebrate: *
14: sp_unclassified: *
15: sp_virus: *
16: sp_bacteriap: *
17: sp_archaeap: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	29	20.6	25	4 Q96QF2	Q96QF2 homo sapien
2	29	20.6	25	15 Q9PXH2	Q9PXH2 human t-lym
3	28	19.9	25	10 Q9C5B6	Q9C5B6 arabidopsis
4	28	19.9	25	10 Q42086	Q42086 arabidopsis
5	27	19.1	25	2 Q47669	Q47669 escherichia
6	27	19.1	25	4 Q16498	Q16498 homo sapien
7	27	19.1	25	12 Q69148	Q69148 human hepe
8	27	19.1	25	15 Q9PXH3	Q9PXH3 human t-lym
9	26	18.4	25	2 O07916	O07916 mycobacteri
10	26	18.4	25	4 Q9UCQ0	Q9UCQ0 homo sapien
11	26	18.4	25	6 Q77605	Q77605 mandrilus
12	26	18.4	25	6 Q77602	Q77602 papio anubi
13	26	18.4	25	6 Q77806	Q77806 mandrilus
14	26	18.4	25	6 Q77827	Q77827 lophocobus
15	26	18.4	25	6 Q77828	Q77828 cercocobus
16	26	18.4	25	6 Q77603	Q77603 theropithec

17	26	18.4	25	6 Q77829	Q77829 cercocobus
18	26	18.4	25	6 Q77607	Q77607 lophocobus
19	26	18.4	25	13 Q91852	Q91852 xenopus lae
20	25	17.7	25	10 Q988V8	Q988V8 triticum ae
21	25	17.7	25	12 Q9PXQ8	Q9PXQ8 foot-and-mo
22	25	17.7	25	13 Q9PRL7	Q9PRL7 xenopus lae
23	24	17.0	25	6 Q8M111	Q8M111 bos taurus
24	24	17.0	25	6 Q9TR43	Q9TR43 bos taurus
25	24	17.0	25	9 Q7Y5L8	Q7Y5L8 bacterioph
26	23	16.3	25	6 Q9TRY2	Q9TRY2 sus sp. ins
27	23	16.3	25	6 Q9TRV5	Q9TRV5 bos taurus
28	23	16.3	25	6 Q9TU61	Q9TU61 gorilla gor
29	23	16.3	25	8 Q33292	Q33292 zea mays (m
30	23	16.3	25	10 Q39915	Q39915 gossypium r
31	23	16.3	25	10 Q39914	Q39914 gossypium r
32	23	16.3	25	15 Q9WRES	Q9WRES human immun
33	22	15.6	25	3 Q96V10	Q96V10 cryptococcu
34	22	15.6	25	5 Q9TWX5	Q9TWX5 hirudinaria
35	22	15.6	25	5 Q9TWX4	Q9TWX4 hirudinaria
36	22	15.6	25	10 Q94EL7	Q94EL7 crobranche c
37	22	15.6	25	15 Q71920	Q71920 human immun
38	22	15.6	25	15 Q71887	Q71887 human immun
39	22	15.6	25	15 Q71946	Q71946 human immun
40	22	15.6	25	15 Q71913	Q71913 human immun
41	22	15.6	25	15 Q99BP7	Q99BP7 human immun
42	22	15.6	25	15 Q71906	Q71906 human immun
43	22	15.6	25	15 Q71981	Q71981 human immun
44	22	15.6	25	15 Q91QP7	Q91QP7 human immun
45	22	15.6	25	15 Q71975	Q71975 human immun

ALIGNMENTS

RESULT 1

Q96QF2 ID Q96QF2 PRELIMINARY; PRT; 25 AA.
AC Q96QF2;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Ovarian/breast septin epsilon (fragment).
GN OV/BR SEPTIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA McIlhannon M.A.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Johnston P.G., Burrows J.F., Donaghy P.G., Chanduloy S.,
RA Johnston P.G., Russell H.;
RT "Genomic organisation, complex splicing pattern and expression of a
RT human septin gene on chromosome 17q25.3".
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ312323; CAC42225.1; -.
FT NON TER 25
SQ SEQUENCE 25 AA; 2642 MW; CD16AC8D55A364F7 CRC64;

Query Match 20.6%; Score 29; DB 4; Length 25;
Best Local Similarity 83.3%; Pred. No. 3.2e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 18 GDSGGP 23
|||
Db 20 GDSGGP 25

RESULT 2

Q9PXH2

```

ID QPXR2 PRELIMINARY; PRT; 25 AA.
AC QPXR2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Variant transactivation factor (Fragment).
OS Human T-lymphotropic virus 1.
OC Viruses; Retroviridae; Retroviridae; Deltairetrovirus.
OC NCBI_TaxID=11908;
RN [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=95191051; PubMed=7533860;
RX Newlesk S., Daenke S., Parker C.E., Taylor G., Weber J.,
RA Nightingale S., Bangham C.R.;
RT "Naturally occurring variants of human T-cell leukemia virus type I
RT Tax protein impair its recognition by cytotoxic T lymphocytes and the
RT transactivation function of Tax.";
RL J. Virol. 69:2649-2653(1995).
DR GO: GO:0016563; F:transcriptional activator activity; IEA.
DR GO: GO:0045941; P:positive regulation of transcription; IEA.
DR InterPro: IPR004120; Tax.
DR Pfam: PF02959; Tax. 1
SQ SEQUENCE 25 AA; 2638 MW; CPOFB04DBBB51D26 CRC64;

Query Match 20.8%; Score 29; DB 15; Length 25;
Best Local Similarity 50.0%; Pred. No. 3.2e+03;
Matches 7; Conservative 1; Mismatches 2; Indels 4; Gaps 1;

QY 13 GDACEGD---SGG 22
DB 1 GDCVQGDWCPVSG 14

RESULT 3
Q9CSB6 PRELIMINARY; PRT; 25 AA.
AC Q9CSB6;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Proline biosynthesis enzyme (Fragment).
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OC NCBI_TaxID=3702;
RN [1]
RN SEQUENCE FROM N.A.
RP Avila C.;
RT "Genes responding to phosphate starvation placed together in
RT Arabidopsis genome.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ275979; CAC35357.1; -.
FT NON-TER 1
SQ SEQUENCE 25 AA; 2712 MW; D3A46D69F94B5D76 CRC64;

Query Match 19.9%; Score 28; DB 10; Length 25;
Best Local Similarity 40.0%; Pred. No. 4.5e+03;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 12 RGDACEGDSG 21
DB 4 KGQVVDGDN 13

RESULT 4
Q42086 PRELIMINARY; PRT; 25 AA.
ID Q42086
AC Q42086;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Glycine-rich RNA binding protein (Fragment).

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OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OC NCBI_TaxID=3702;
RN [1]
RN SEQUENCE FROM N.A.
RP STRAIN=cv. Columbia;
RA Phillipps G., Gigot C.;
RL Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z26410; CAA81244.1; -.
FT NON-TER 1
SQ SEQUENCE 25 AA; 2421 MW; E1064170E1E33751 CRC64;

Query Match 19.9%; Score 28; DB 10; Length 25;
Best Local Similarity 71.4%; Pred. No. 4.5e+03;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 18 GDGSGGPF 24
DB 19 GDGSGGPF 25

RESULT 5
Q47669 PRELIMINARY; PRT; 25 AA.
ID Q47669
AC Q47669;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE TrpA46-Asp-PR3 protein (Fragment).
GN TrpA46-Asp-PR3
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OC NCBI_TaxID=562;
RN [1]
RN SEQUENCE FROM N.A.
RP STRAIN-K-12;
RX MEDLINE=89323228; PubMed=2502189;
RT Tucker S.D., Murgola E.J., Pögel F.T.;
RT "Missense and nonsense suppressors can correct frameshift mutations.";
RL Biochimie 71:729-739(1989).
DR EMBL; X16698; CAA34671.1; -.
FT NON-TER 1
SQ SEQUENCE 25 AA; 2759 MW; 93B6A5FDAE24C8D8 CRC64;

Query Match 19.1%; Score 27; DB 2; Length 25;
Best Local Similarity 40.0%; Pred. No. 6.3e+03;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 5 YKPDEGKGGD 14
DB 16 FRPGSGKSSD 25

RESULT 6
Q16498 PRELIMINARY; PRT; 25 AA.
ID Q16498
AC Q16498;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE GM-CSF receptor alpha subunit (Fragment).
GN CSF2RA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=93052350; PubMed=1358805;
RX Rappold G., Willson T.A., Henke A., Gough N.M.;

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RT "Arrangement and localization of the human GM-CSF receptor alpha chain
gene CSF2RA within the X-Y pseudoautosomal region.";
RL Genomics 14:455-461(1992).
DR EMBL; S48539; AAB23942.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
FT RECEPTOR.
KW NON_TER 25 25
SQ SEQUENCE 25 AA; 3014 MW; 3A5827B3BF28E35E CRC64;
Query Match 19.1%; Score 27; DB 4; Length 25;
Best Local Similarity 57.1%; Pred. No. 6.3e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 5 YKPDGK 11
Db : : : : :
Db 6 FTPEGK 12
RESULT 7
Q69148 PRELIMINARY; PRT; 25 AA.
AC Q69148;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE W1 protein (Fragment).
GN W1.
OS Human herpesvirus 4 (Epstein-Barr virus).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae; Lymphocryptovirus.
OX NCBI_TaxID=10376;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89020826; PubMed=2845663;
RA Sauter M., Boos H., Hirsch P., Mueller-Lantzsch N.;
RT "Characterization of a Latent Protein Encoded by the Large Internal
Repeats and the BamHI Y Fragment of the Epstein-Barr (EBV) Genome.";
RL Virology 166:586-590(1988).
DR EMBL; M23259; AAA45904.1; -.
DR InterPro; IPR005030; Herpes_LP.
DR Pfam; PF03363; Herpes_LP; 1.
FT NON_TER 1
SQ SEQUENCE 25 AA; 2443 MW; 32530AA49468B8E13 CRC64;
Query Match 19.1%; Score 27; DB 12; Length 25;
Best Local Similarity 58.3%; Pred. No. 6.3e+03;
Matches 7; Conservative 0; Mismatches 3; Indels 2; Gaps 1;
QY 12 RGDACGDSGGP 23
Db : : : : :
Db 1 RGDSEGP--GP 10
RESULT 8
Q9PXH3 PRELIMINARY; PRT; 25 AA.
AC Q9PXH3;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Variant transactivation factor (Fragment).
OS Human T-lymphotropic virus 1.
OC Viruses; Retroid viruses; Retroviridae; Deltaretrovirus.
OX NCBI_TaxID=11908;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95191051; PubMed=7533860;
RA Newlesk S., Daenke S., Parker C.E., Taylor G., Weber J.,
RA Nightingale S., Bangham C.R.;
RT "Naturally occurring variants of human T-cell leukemia virus type I
Tax protein impair its recognition by cytotoxic T lymphocytes and the
transactivation function of Tax.";
RL J. Virol. 69:2649-2653(1995).

DR GO; GO:0016563; F:transcriptional activator activity; IEA.
DR GO; GO:0045341; P:positive regulation of transcription; IEA.
DR InterPro; IPR004120; Tax.
DR Pfam; PF02959; Tax; 1.
SQ SEQUENCE 25 AA; 2712 MW; 950FBD4DBBBS155F CRC64;
Query Match 19.1%; Score 27; DB 15; Length 25;
Best Local Similarity 50.0%; Pred. No. 6.3e+03;
Matches 7; Conservative 1; Mismatches 2; Indels 4; Gaps 1;
QY 13 GDACEGD---SGG 22
Db : : : : :
Db 1 GDYVQGDWCPISGG 14
RESULT 9
O07916 PRELIMINARY; PRT; 25 AA.
AC O07916;
DT 01-JUL-1997 (TREMBlrel. 04, Created)
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mycobacterium tuberculosis, and
OS Mycobacterium tuberculosis, and
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773; 33892;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=2296207, and PASTEUR;
RA Supply P., Magdalena J., Himpens S., Loch C.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y13628; CAA73960.1; -.
DR EMBL; Y13627; CAA73955.1; -.
DR EMBL; Y13628; CAA73959.1; -.
KW Hypothetical protein.
SQ SEQUENCE 25 AA; 2639 MW; 036E7271A33D1CF2 CRC64;
Query Match 18.4%; Score 26; DB 2; Length 25;
Best Local Similarity 33.3%; Pred. No. 8.8e+03;
Matches 6; Conservative 3; Mismatches 3; Indels 6; Gaps 1;
QY 8 DEGKRGD-----ACBGD 19
Db : : : : :
Db 6 DDAERSDEVGAPPACGGE 23
RESULT 10
Q9UCQ0 PRELIMINARY; PRT; 25 AA.
AC Q9UCQ0;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE KU antigen 84 kDa protein fraction 15 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=32165807; PubMed=1537839;
RA Wedrychowski A., Henzel W., Huston L., Paslidis N., Ellerson D.,
RA McRae M., Seong D., Howard O.M., Daissiroth A.;
RT "Identification of proteins binding to interferon-inducible
transcriptional enhancers in hematopoietic cells.";
RL J. Biol. Chem. 267:4533-4540(1992).
DR PIR; D42397; D42397.
DR GO; GO:0003677; F:DNA binding; NAS.
FT NON_TER 1
FT NON_TER 1
FT NON_TER 25 25
SQ SEQUENCE 25 AA; 2550 MW; 9976496E6105DC69 CRC64;

Query Match 18.4%; Score 26; DB 4; Length 25;
 Best Local Similarity 43.8%; Pred. No. 8.8e+03;
 Matches 7; Conservative 2; Mismatches 5; Indels 1;

QY 9 EGRKGD-ACEGDSGG 22
 DB 1 DFGSGDTAAVEFEFG 16

RESULT 11

ID O77605 PRELIMINARY; PRT; 25 AA.
 AC O77605;
 DT 01-NOV-1998 (TReMBLrel. 08, Created)
 DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
 DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)
 DE Testis specific protein (Fragment).
 OS Mandrillus leucophaeus (Prill) (Papio leucophaeus).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Mandrillus.
 OX NCBI_TaxID=9556;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Harris E.E., Disotell T.R.;
 RT "Nuclear Gene Trees and the Phylogenetic Relationships of the
 RT Mangabeys (Primates: Papionini).";
 RL Mol. Biol. Evol. 0:0-0(1998).
 DR EMBL; AF057421; AAC25149.1; -.
 FT NON_TER 1
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 25 AA; 2799 MW; A50DAC7A60359098 CRC64;

Query Match 18.4%; Score 26; DB 6; Length 25;
 Best Local Similarity 37.5%; Pred. No. 8.8e+03;
 Matches 6; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 6 KPDEGKRGDACEGDSG 21
 DB 1 KPDLDRGAIQGMFG 16

RESULT 12

ID O77602 PRELIMINARY; PRT; 25 AA.
 AC O77602;
 DT 01-NOV-1998 (TReMBLrel. 08, Created)
 DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
 DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)
 DE Testis specific protein (Fragment).
 OS Papio anubis (Olive baboon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Papio.
 OX NCBI_TaxID=9555;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Harris E.E., Disotell T.R.;
 RT "Nuclear Gene Trees and the Phylogenetic Relationships of the
 RT Mangabeys (Primates: Papionini).";
 RL Mol. Biol. Evol. 0:0-0(1998).
 DR EMBL; AF057408; AAC25136.1; -.
 FT NON_TER 1
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 25 AA; 2799 MW; A50DAC7A60359098 CRC64;

Query Match 18.4%; Score 26; DB 6; Length 25;
 Best Local Similarity 37.5%; Pred. No. 8.8e+03;
 Matches 6; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 6 KPDEGKRGDACEGDSG 21
 DB 1 KPDLDRGAIQGMFG 16

Db 1 KPDLDRGAIQGMFG 16

RESULT 13

ID O77606 PRELIMINARY; PRT; 25 AA.
 AC O77606;
 DT 01-NOV-1998 (TReMBLrel. 08, Created)
 DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
 DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)
 DE Testis specific protein (Fragment).
 OS Mandrillus sphinx (Mandrill) (Papio sphinx).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Mandrillus.
 OX NCBI_TaxID=9561;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Harris E.E., Disotell T.R.;
 RT "Nuclear Gene Trees and the Phylogenetic Relationships of the
 RT Mangabeys (Primates: Papionini).";
 RL Mol. Biol. Evol. 0:0-0(1998).
 DR EMBL; AF057422; AAC25150.1; -.
 FT NON_TER 1
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 25 AA; 2799 MW; A50DAC7A60359098 CRC64;

Query Match 18.4%; Score 26; DB 6; Length 25;
 Best Local Similarity 37.5%; Pred. No. 8.8e+03;
 Matches 6; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 6 KPDEGKRGDACEGDSG 21
 DB 1 KPDLDRGAIQGMFG 16

RESULT 14

ID O77827 PRELIMINARY; PRT; 25 AA.
 AC O77827;
 DT 01-NOV-1998 (TReMBLrel. 08, Created)
 DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
 DT 01-OCT-2001 (TReMBLrel. 18, Last annotation update)
 DE Testis specific protein (Fragment).
 OS Lophocebus albigena albigena.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Lophocebus.
 OX NCBI_TaxID=75568;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN-SYLVAIN, and SAKI;
 RA Harris E.E., Disotell T.R.;
 RT "Nuclear Gene Trees and the Phylogenetic Relationships of the
 RT Mangabeys (Primates: Papionini).";
 RL Mol. Biol. Evol. 0:0-0(1998).
 DR EMBL; AF057425; AAC25153.1; -.
 DR EMBL; AF057424; AAC25152.1; -.
 FT NON_TER 1
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 25 AA; 2799 MW; A50DAC7A60359098 CRC64;

Query Match 18.4%; Score 26; DB 6; Length 25;
 Best Local Similarity 37.5%; Pred. No. 8.8e+03;
 Matches 6; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 6 KPDEGKRGDACEGDSG 21
 DB 1 KPDLDRGAIQGMFG 16

RESULT 15

O77828

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ID O77828 PRELIMINARY; PRT; 25 AA.
AC O77828;
DT 01-NOV-1998 (TRENBLrel. 08, Created)
DT 01-NOV-1998 (TRENBLrel. 08, Last sequence update)
DT 01-OCT-2001 (TRENBLrel. 18, Last annotation update)
DE Testis specific protein (Fragment).
OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Cercopithecidae;
OX NCBI_TaxID=9531;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CTL941, CTL926, CTA078, and F105;
RA Harris E.E., Disotell T.R.;
RT "Nuclear Gene Trees and the Phylogenetic Relationships of the
RT Mangabeys (Primates: Papionini).";
RL MCL. Biol. Evol. 0:0-0(1998).
DR EMBL; AF057414; AAC25142.1; -.
DR EMBL; AF057411; AAC25139.1; -.
DR EMBL; AF057412; AAC25140.1; -.
DR EMBL; AF057413; AAC25141.1; -.
FT NON_TER 1
FT NON_TER 25
SQ SEQUENCE 25 AA; 2799 MW; A50DAC7A60359098 CRC64;

Query Match 18.4%; Score 26; DB 6; Length 25;
Best Local Similarity 37.5%; Pred. No. 8.8e+03;
Matches 6; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 6 KPDEGKRGDACEGDSG 21
Db 1 KPDLDRRGAIQMPG 16

```

Search completed: February 26, 2004, 09:49:36
Job time : 42 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 26, 2004, 09:42:37 ; Search time 51 Seconds
(without alignments)
138.504 Million cell updates/sec

Title: US-09-909-348-5

Perfect score: 141

Sequence: 1 AGTRYKPDGKRGDACEGSGGPFV 25

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 7982

Minimum DB seq length: 25

Maximum DB seq length: 25

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Genesep 29Jan04:*

1: genesep1980s:*

2: genesep1990s:*

3: genesep2000s:*

4: genesep2001s:*

5: genesep2002s:*

6: genesep2003as:*

7: genesep2003bs:*

8: genesep2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	25.5	25	4	AAM17856
2	36	25.5	25	4	AB36874 Peptide #
3	36	25.5	25	4	AAM30362
4	36	25.5	25	4	AB31661 Peptide #
5	36	25.5	25	4	AB31661 Peptide #
6	36	25.5	25	4	AB22200 Protein #
7	36	25.5	25	4	AAM70024 Human bon
8	36	25.5	25	4	AAM57620 Human bon
9	36	25.5	25	4	ABG51720 Human liv
10	36	25.5	25	5	AAM05503 Peptide #
11	34	24.1	25	4	ABG39654 Human pep
12	33	23.4	25	4	ABG66984 Mutant pr
13	33	23.4	25	4	AB38532 Peptide #
14	33	23.4	25	4	AAM31981 Peptide #
15	33	23.4	25	4	AAM71690 Human bon
16	33	23.4	25	4	AAM59154 Human bra
17	33	23.4	25	4	ABG53374 Human liv
18	31.5	22.3	25	5	ABG41503 Human pep
19	31	22.0	25	5	ADC99395 Peptide i
20	31	22.0	25	5	AAM06631 Insulin/i
21	30	21.3	25	6	ADA04468 IGF-1R re
22	30	21.3	25	2	AAM40290 Human con
23	30	21.3	25	2	AAY06185 Anti-angi
24	30	21.3	25	2	AAM88795 Polypepti
25	30	21.3	25	4	AB50650 Human sec
				6	AAM16503 Synthetic

26	30	21.3	25	6	ABO44907	Novel hum
27	30	21.3	25	7	ABO26387	Protein a
28	29	20.6	25	1	AAP30093	CD4 anti-
29	29	20.6	25	2	AAR29089	Generic p
30	29	20.6	25	2	AAR56963	Linker pe
31	29	20.6	25	2	AAM10259	Hepatitis
32	29	20.6	25	2	AAM97179	Linker us
33	29	20.6	25	2	AAV05761	Single ch
34	29	20.6	25	2	AAV36640	Fragment
35	29	20.6	25	4	AAM50156	MAB 9A4 s
36	29	20.6	25	6	AAO16697	Anti-ovar
37	29	20.6	25	6	AAO16508	Synthetic
38	28.5	20.2	25	6	ADA11881	Human nov
39	28.5	20.2	25	2	AAM52207	Interleuk
40	28	19.9	25	2	AAM49114	Human leu
41	28	19.9	25	2	AAW78292	Fragment
42	28	19.9	25	4	ABBA3355	Peptide #
43	28	19.9	25	4	AAM37208	Peptide #
44	28	19.9	25	4	AAM77088	Human bon
45	28	19.9	25	4	AAO08556	Human pol

ALIGNMENTS

RESULT 1
AAM17856
ID AAM17856 standard; protein; 25 AA.
XX AC AAM17856;
XX DT 12-OCT-2001 (first entry)
DE Peptide #4290 encoded by probe for measuring cervical gene expression.
KW Probe; human; microarray; gene expression; cervical epithelial cell;
KW cervical cancer.
XX OS Homo sapiens.
XX FN WO200157278-A2.
PD 09-AUG-2001.
PF 30-JAN-2001; 2001WO-US000670.
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
PA Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488901/53.
XX Human genome-derived single exon nucleic acid probes useful for analyzing
XX Gene expression in human cervical epithelial cells.
XX Claim 27; SEQ ID NO 22682; 487pp; English.

The present invention relates to human single exon nucleic acid probes (SENPs; see AAI10068-AI28459). The present sequence is a peptide encoded by one such probe. The SENPs are derived from human Hela cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer. Note: The sequence data for this patent did not form

CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 25 AA;

Query Match 25.5%; Score 36; DB 4; Length 25;
Best Local Similarity 66.7%; Pred. No. 1.9e+03;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 15 ACEGDSGGP 23
Db 11 ACQSRSGGP 19

RESULT 2
ABB36874
ID ABB36874 standard; peptide; 25 AA.

XX ABB36874;
AC ABB36874;
XX
DT 04-FEB-2002 (first entry)
XX
DE Peptide #4380 encoded by human foetal liver single exon probe.
XX
KW Human; foetal liver; gene expression; single exon nucleic acid probe.
XX
OS Homo sapiens.
XX
FN WO200157277-A2.
XX
PD 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US000669.

XX 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-483447/52.

XX Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human foetal liver.

XX Claim 27; SEQ ID NO 29509; 639pp + Sequence Listing; English.

XX The invention relates to a single exon nucleic acid probe for measuring
CC human gene expression in a sample derived from human foetal liver. The
CC single exon nucleic acid probes may be used for predicting, measuring and
CC displaying gene expression in samples derived from human foetal liver. The
CC present sequence is a peptide encoded by a single exon nucleic acid probe
CC of the invention. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 25 AA;

Query Match 25.5%; Score 36; DB 4; Length 25;
Best Local Similarity 66.7%; Pred. No. 1.9e+03;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 15 ACEGDSGGP 23
Db 11 ACQSRSGGP 19

RESULT 3
AAM30362

ID AAM30362 standard; protein; 25 AA.

XX AAM30362;

XX 17-OCT-2001 (first entry)

XX Peptide #4399 encoded by probe for measuring placental gene expression.

XX Probe; microarray; human; placenta; antenatal diagnosis;
KW genetic disorder.

XX Homo sapiens.

XX WO200157272-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US000663.

XX 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488897/53.

XX Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human placenta.

XX Claim 27; SEQ ID NO 30631; 654pp; English.

XX The present invention relates to single exon nucleic acid probes (SENP:
CC see AAI31315-AAI57546). The present sequence is a peptide encoded by one
CC such probe. The probes are useful for producing a microarray for
CC predicting, measuring and displaying gene expression in samples derived
CC from human placenta. The probes are useful for antenatal diagnosis of
CC human genetic disorders

XX Sequence 25 AA;

Query Match 25.5%; Score 36; DB 4; Length 25;
Best Local Similarity 66.7%; Pred. No. 1.9e+03;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 15 ACEGDSGGP 23
Db 11 ACQSRSGGP 19

RESULT 4
ABB31661

ID ABB31661 standard; peptide; 25 AA.

XX ABB31661;

XX 01-FEB-2002 (first entry)

XX Peptide #4312 encoded by breast cell single exon nucleic acid probe.

XX Human; microarray; single exon probe; gene expression; breast; disease;
KW cancer.

XX Homo sapiens.

XX

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PN WO200157271-A2.
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US000662.
XX
XX 04-FEB-2000; 2000US-0180312P.
XX 26-MAY-2000; 2000US-0207456P.
XX 30-JUN-2000; 2000US-00608408.
XX 03-AUG-2000; 2000US-00632366.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-496933/54.
XX
XX New spatially-addressable set of single exon nucleic acid probes, useful
XX for measuring gene expression in sample derived from human breast,
XX comprises number of single exon nucleic acid probes.
XX
XX Claim 27; SEQ ID NO 14629; 327pp + Sequence Listing; English.
XX
XX The invention relates to a spatially-addressable set of single exon
XX nucleic acid probes for measuring gene expression in a sample derived
XX from human breast and BT 474 cells. The method involves contacting the
XX probes with a collection of detectably labelled nucleic acids derived
XX from mRNA of human breast, and then measuring the label bound to each
XX probe of the microarray. The probes are useful for verifying the
XX expression of regions of genomic DNA predicted to encode proteins. They
XX are useful for gene discovery, and for determining predisposition and/or
XX prognosing breast disease. Gene expression analysis is useful for
XX assessing the toxicity of chemical agents on cells. The microarray of
XX this invention presents a far greater diversity of probes for measuring
XX gene expression, with far less bias than expressed sequence tag
XX microarrays. The method is suitable for rapid production of functional
XX information from genomic sequence. The present sequence is a peptide
XX encoded by a single exon nucleic acid probe of the invention. Note: The
XX sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 25 AA;
SQ
Query Match 25.5%; Score 36; DB 4; Length 25;
Best Local Similarity 56.7%; Pred. NO. 1.9e+03;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
OY 15 ACEGDSGGP 23
Db 11 ACQSRSGGP 19
RESULT 5
ABB22200
ID ABB22200 standard; protein; 25 AA.
XX
XX ABB22200;
XX
XX 23-JAN-2002 (first entry)
XX
XX Protein #4199 encoded by probe for measuring heart cell gene expression.
XX Human; gene expression; heart; microarray; vascular system;
XX cardiovascular disease; hypertension; cardiac arrhythmia;
XX congenital heart disease.
XX
XX Homo sapiens.
XX
XX WO200157274-A2.

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XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US000666.
XX
XX 04-FEB-2000; 2000US-0180312P.
XX 26-MAY-2000; 2000US-0207456P.
XX 30-JUN-2000; 2000US-00608408.
XX 03-AUG-2000; 2000US-00632366.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488899/53.
XX
XX Single exon nucleic acid probes for analyzing gene expression in human
XX hearts.
XX
XX Claim 15; SEQ ID NO 23970; 530pp; English.
XX
XX The present invention relates to single exon nucleic acid probes for
XX measuring human gene expression in a sample derived from human heart (see
XX AB21535-ABA41305). The present sequence is a protein encoded by one such
XX probe. The probes may be used for predicting, measuring and displaying
XX gene expression in samples derived from the human heart via microarrays.
XX By measuring gene expression, the probes are useful for predicting,
XX diagnosing, grading, staging, monitoring and prognosing diseases of the
XX human heart and vascular system e.g. cardiovascular disease,
XX hypertension, cardiac arrhythmias and congenital heart disease. Note: The
XX sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 25 AA;
SQ
Query Match 25.5%; Score 36; DB 4; Length 25;
Best Local Similarity 66.7%; Pred. NO. 1.9e+03;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
OY 15 ACEGDSGGP 23
Db 11 ACQSRSGGP 19
RESULT 6
AAM70024
ID AAM70024 standard; protein; 25 AA.
XX
XX AAM70024;
XX
XX 06-NOV-2001 (first entry)
XX
XX Human bone marrow expressed probe encoded protein SEQ ID NO: 30330.
XX
XX Human; bone marrow expressed exon; gene expression analysis; probe;
XX microarray; cancer; leukaemia; lymphoma; myeloma.
XX
XX Homo sapiens.
XX
XX WO200157276-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US000668.
XX
XX 04-FEB-2000; 2000US-0180312P.
XX 26-MAY-2000; 2000US-0207456P.
XX 30-JUN-2000; 2000US-00608408.
XX 03-AUG-2000; 2000US-00632366.
XX
XX Homo sapiens.
XX
XX WO200157274-A2.

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PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-488900/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for analyzing
XX PT gene expression in human bone marrow.
XX
XX Example 4; SEQ ID NO 30330; 658pp + Sequence Listing; English.
XX
XX The present invention provides a number of single exon nucleic acid
XX CC probes which are derived from genomic sequences expressed in the human
XX CC bone marrow. They can be used to measure gene expression in bone marrow
XX CC samples, which may enable the improved diagnosis and treatment of cancers
XX CC such as lymphoma, leukaemia and myeloma. The present sequence is a
XX CC protein encoded by one of the probes of the invention
XX
XX Sequence 25 AA;
XX
XX Query Match 25.5%; Score 36; DB 4; Length 25;
XX Best Local Similarity 66.7%; Pred. No. 1.9e+03;
XX Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0
XX
QY 15 ACEGDSGGP 23
DB ||: ||||
  11 ACQSRSGGP 19
XX
RESULT 7
AAMS7620
ID AAMS7620 standard; protein; 25 AA.
XX
XX AAMS7620;
XX
XX 05-NOV-2001 (first entry)
XX
XX Human brain expressed single exon probe encoded protein SEQ ID NO: 29725.
XX
XX Human; brain expressed exon; gene expression analysis; probe; microarray;
XX KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
XX
XX Homo sapiens.
XX
XX WO200157275-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US0000667.
XX
XX 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-483446/52.
XX
XX Single exon nucleic acid probes for analyzing gene expression in human
XX PT brains.
XX
XX Example 4; SEQ ID NO 29725; 650pp + Sequence Listing; English.
XX
XX

```

XX SQ Sequence 25 AA;
 Query Match 25.5%; Score 36; DB 4; Length 25;
 Best Local Similarity 66.7%; Pred. No. 1.9e+03;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 15 AREGDSGGP 23
 ||: |||||
 Db 11 ACQSRSGGP 19
 ||: |||||
 Db 11 ACQSRSGGP 19
 ||: |||||
 RESULT 9
 AAM05503
 ID AAM05503 standard; protein; 25 AA.
 AC AAM05503;
 XX
 XX
 DT 09-OCT-2001 (first entry)
 DE Peptide #4185 encoded by probe for measuring breast gene expression.
 XX Probe; human; breast disease; breast cancer; development disorder;
 KW inflammatory disease; proliferative breast disease; non-carcinoma tumour.
 KW
 XX Homo sapiens.
 OS
 XX
 PN WO200157270-A2.
 XX
 XX 09-AUG-2001.
 XX
 XX 29-JAN-2001; 2001WO-US000661.
 XX
 XX 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 PA
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 PI
 XX WPI; 2001-476286/51.
 XX
 XX Novel single exon nucleic acid probe used to measuring gene expression in
 PT a human breast.
 PT
 XX
 XX Claim 27; SEQ ID NO 14243; 322pp; English.
 XX
 XX The present invention relates to novel single exon nucleic acid probes
 CC (see AAI00010-AA110067). The present sequence is a peptide encoded by one
 CC such probe. The probes are useful for measuring human gene expression in
 CC a human breast sample, where the probe hybridises at high stringency to a
 CC nucleic acid expressed in the human breast. The probes are useful for
 CC predicting, diagnosing, grading, staging, monitoring and prognosing
 CC diseases of the human breast, particularly those diseases with polygenic
 CC aetiology. The diseases include: breast cancer, disorders of development,
 CC inflammatory diseases of the breast, fibrocytic changes, proliferative
 CC breast disease and non-carcinoma tumours. Note: The sequence data for
 CC this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 25 AA;
 Query Match 25.5%; Score 36; DB 4; Length 25;
 Best Local Similarity 66.7%; Pred. No. 1.9e+03;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 15 AREGDSGGP 23
 ||: |||||
 Db 11 ACQSRSGGP 19
 ||: |||||

Db 11 ACQSRSGGP 19
 ||: |||||
 RESULT 10
 ABG39654
 ID ABG39654 standard; peptide; 25 AA.
 XX
 XX ABG39654;
 XX
 DT 19-AUG-2002 (first entry)
 DE Human peptide encoded by genome-derived single exon probe SEQ ID 29319.
 XX
 XX Human; single exon probe; asthma; lung cancer; COPD; ILD;
 KW chronic obstructive pulmonary disease; interstitial lung disease;
 KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
 KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
 KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
 KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagenen syndrome;
 KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
 KW primary ciliary dyskinesia; pulmonary hypertension;
 KW hyaline membrane disease.
 KW
 XX Homo sapiens.
 OS
 XX
 PN WO200186003-A2.
 XX
 XX 15-NOV-2001.
 XX
 XX 30-JAN-2001; 2001WO-US000665.
 XX
 XX 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 PA
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 PI
 XX WPI; 2002-114183/15.
 XX
 XX Spatially-addressable set of single exon nucleic acid probes, used to
 PT measure gene expression in human lung samples.
 PT
 XX
 XX Claim 27; SEQ ID NO 29319; 634pp; English.
 XX
 XX The invention relates to a spatially-addressable set of single exon
 CC nucleic acid probes for measuring gene expression in a sample derived
 CC from human lung comprising single exon nucleic acid probes having one of
 CC 12814 nucleic acid sequences mentioned in the specification, or their
 CC complements or the 12387 open reading frames derived from the 12614
 CC probes. Also included are a microarray comprising the novel set of probes
 CC; the novel set of probes which hybridise at high stringency to a nucleic
 CC acid expressed in the human lung; measuring gene expression in a sample
 CC derived from human lung, comprising (a) contacting the array with a
 CC collection of detectably labeled nucleic acids derived from human lung
 CC mRNA, and (b) measuring the label detectably bound to each probe of the
 CC array; identifying exons in a eukaryotic genome, comprising (a)
 CC algorithmically predicting at least one exon from genomic sequences of
 CC the eukaryote; and (b) detecting specific hybridisation of detectably
 CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
 CC having a fragment identical to the predicted exon, the probe is included
 CC in the above mentioned microarray; assigning exons to a single gene,
 CC comprising (a) identifying exons from genomic sequence by the method
 CC above and (b) measuring the expression of each of the exons in several
 CC tissues and/or cell types using hybridisation to a single exon
 CC microarrays having a probe with the exon, where a common pattern of
 CC expression of the exons in the tissues and/or cell types indicates that

CC the exons should be assigned to a single gene; a peptide comprising one
 CC of 12011 sequences, mentioned in the specification, or encoded by the
 CC probes/open reading frames (ORF). The probes are used for gene expression
 CC analysis, and for identifying exons in a gene, particularly using human
 CC lung derived mRNA and for the study of lung diseases such as asthma, lung
 CC cancer, chronic obstructive pulmonary disease (COPD), interstitial lung
 CC disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,
 CC tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-
 CC Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary
 CC histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,
 CC Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary
 CC dyskinesia, pulmonary hypertension and hyaline membrane disease. The
 CC present sequence is a peptide/protein encoded by a single exon probe of
 CC the invention. Note: the sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 25 AA;
 Query Match 25.5%; Score 36; DB 5; Length 25;
 Best Local Similarity 66.7%; Pred. No. 1.9e+03;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 15 ACEGDSGGP 23
 ||: ||||
 Db 11 ACQSRGGP 19

RESULT 11
 AAG66984
 ID AAG66984 standard; peptide; 25 AA.
 AC AAG66984;
 XX
 XX 29-OCT-2001 (first entry)
 DT
 DE Mutant preproliferin linker region of PAP324 (MMP-9).
 XX
 XX Castor oil plant; ricin; preproliferin; cytostatic; antiinflammatory;
 KW antirheumatic; antiarthritic; antiarteriosclerotic; neuroprotective;
 KW toxin; linker; protease-specific cleavage site; cancer;
 KW inflammatory disease; mutant; variant; matrix metalloproteinase 9; MMP-9;
 KW UPA.

XX Ricinus communis.
 OS Synthetic.
 OS
 XX WO200125267-A2.
 XX
 XX 12-APR-2001.
 PD
 XX 04-OCT-2000; 2000WO-CA001162.
 PF
 XX 04-OCT-1999; 99US-0157807P.
 PR
 XX 14-APR-2000; 2000US-0197409P.
 XX
 XX (TWIN-) TWINSTRAND THERAPEUTICS INC.
 PA
 XX Braun C, Purac A, Borgford T;
 PI
 XX WPI; 2001-300164/31.
 DR

XX New proteins comprising A and B chains of ricin-like toxin linked by a
 PT novel linker sequence that is specifically cleaved and activated by
 PT protease specific to cancer is useful for treating inflammation and
 PT cancer.
 XX
 XX Claim 42; Fig 17C; 146pp; English.

XX The invention relates to a recombinant protein comprising an A chain of a
 CC ricin-like toxin, a B chain of a ricin-like toxin and a heterologous
 CC linker that links the A and B chains. The linker sequence contains a
 CC cleavage recognition site for a specific protease such as those found in

CC inflammatory cells and cancer cells. The protein is useful for inhibiting
 CC or destroying cells expressing a specific protease, e.g. cancer cells
 CC found in T- and B-cell lymphoproliferative diseases, ovarian cancer,
 CC pancreatic cancer, head and neck cancer, squamous cell carcinoma,
 CC gastrointestinal cancer, breast cancer, prostate cancer or non-small cell
 CC lung cancer, or cells found in rheumatoid arthritis, atherosclerosis,
 CC Crohn's disease or central nervous system disease. The protein is useful
 CC for treating cancer and inflammation. The protein has the specificity for
 CC cells that contain a specific protease, including those of inflammatory
 CC disorders and cancer cells, without the need for a cell binding
 CC component. The present sequence is one of a number of variant linkers
 CC generated from the wild type preproliferin linker. The variant linkers
 CC contain a cleavage recognition site for either matrix metalloproteinase 9
 CC (MMP-9) or UPA

SQ Sequence 25 AA;
 Query Match 24.1%; Score 34; DB 4; Length 25;
 Best Local Similarity 53.8%; Pred. No. 3.3e+03;
 Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 10 GKRGDACGDSGG 22
 ||: ||||
 Db 7 GPQGIAGGSGG 19

RESULT 12
 ABB38532
 ID ABB38532 standard; peptide; 25 AA.
 AC ABB38532;
 XX
 XX 04-FEB-2002 (first entry)
 DT
 DE Peptide #6038 encoded by human foetal liver single exon probe.
 XX
 XX Human; foetal liver; gene expression; single exon nucleic acid probe.
 XX
 XX Homo sapiens.
 OS
 XX WO200157277-A2.
 PN
 XX 09-AUG-2001.
 PD
 XX 30-JAN-2001; 2001WO-US000669.
 PF
 XX 04-FEB-2000; 2000US-0180312P.
 PR
 XX 26-MAY-2000; 2000US-0207456P.
 PR
 XX 30-JUN-2000; 2000US-00608408.
 PR
 XX 03-AUG-2000; 2000US-00632386.
 PR
 XX 21-SEP-2000; 2000US-0234687P.
 PR
 XX 27-SEP-2000; 2000US-0236359P.
 PR
 XX 04-OCT-2000; 2000GB-00024263.
 XX
 XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;
 PI
 XX WPI; 2001-483447/52.
 DR
 XX
 XX Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human fetal liver.
 PT
 XX Claim 27; SEQ ID NO 31167; 639pp + Sequence Listing; English.

XX The invention relates to a single exon nucleic acid probe for measuring
 CC human gene expression in a sample derived from human foetal liver. The
 CC single exon nucleic acid probes may be used for predicting, measuring and
 CC displaying gene expression in samples derived from human foetal liver. The
 CC present sequence is a peptide encoded by a single exon nucleic acid probe
 CC of the invention. Note: The sequence data for this patent did not form
 CC part of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

RESULT 14
AAM71690
ID AAM71690 standard; protein; 25 AA.

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XX 30-JAN-2001; 2001WO-US000667.
PF 04-FEB-2000; 2000US-0180312P.
XX 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
PA Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-483446/52.
XX Single exon nucleic acid probes for analyzing gene expression in human
PT brains.
XX Example 4; SEQ ID NO 31259; 650pp + Sequence Listing; English.
XX The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC brain. They can be used to measure gene expression in brain cell samples,
CC which may enable the diagnosis and improved treatment of nervous system
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is a protein encoded by one of
CC the probes of the invention
XX
XX Sequence 25 AA;
SQ
Query Match 23.4%; Score 33; DB 4; Length 25;
Best Local Similarity 40.0%; Pred.No. 4.3e-03;
Matches 6; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
QY 8 DEGRKGDACBDSGG 22
Db :|||:|:|
10 ECGNQDDEPDHNGG 24
Search completed: February 26, 2004, 09:48:22
Job time : 56 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 26, 2004, 09:49:38 ; Search time 33 Seconds
(without alignments)
159.965 Million cell updates/sec

Title: US-09-909-348-5

Perfect score: 141

Sequence: 1 AGTRYKPDGKRGDACEGDSGGPFV 25

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 809742 seqs, 211153259 residues

Total number of hits satisfying chosen parameters: 2731

Minimum DB seq length: 25

Maximum DB seq length: 25

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications AA:*
- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
 - 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
 - 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
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 - 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
 - 14: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
 - 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
 - 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
 - 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
 - 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	141	100.0	25	9	US-09-909-348-5
2	141	100.0	25	9	US-09-909-122-5
3	141	100.0	25	13	US-10-050-692-5
4	38	27.0	25	15	US-10-353-522A-1
5	36	25.5	25	9	US-09-864-761-37498
6	33	23.4	25	9	US-09-864-761-43492
7	31.5	22.3	25	14	US-10-280-066-233
8	31	22.0	25	10	US-09-852-455-75
9	31	22.0	25	10	US-09-962-756-1099
10	31	22.0	25	14	US-10-133-138-205
11	31	22.0	25	14	US-10-289-660-205
12	31	22.0	25	15	US-10-253-471-1099
13	31	22.0	25	16	US-10-253-493-1099
14	30	21.3	25	10	US-09-933-767-598
15	30	21.3	25	13	US-10-036-869-7

16	30	21.3	25	14	US-10-023-282-598	Sequence 598, App
17	30	21.3	25	15	US-10-448-163-11	Sequence 11, Appl
18	29	20.6	25	14	US-10-897-065-409	Sequence 409, App
19	28	19.9	25	9	US-09-864-761-45944	Sequence 45944, A
20	28	19.9	25	14	US-10-094-401-255	Sequence 255, App
21	28	19.9	25	15	US-10-462-262-219	Sequence 219, Appl
22	27.5	19.5	25	15	US-10-420-559-23	Sequence 23, Appl
23	27	19.1	25	9	US-09-738-970-3	Sequence 3, Appl
24	27	19.1	25	14	US-10-380-066-256	Sequence 256, App
25	27	19.1	25	14	US-10-376-194-3	Sequence 3, Appl
26	27	19.1	25	15	US-10-375-716-32	Sequence 32, Appl
27	26.5	18.8	25	14	US-10-059-261-311	Sequence 311, App
28	26.5	18.8	25	14	US-10-059-261-312	Sequence 312, App
29	26.5	18.8	25	14	US-10-059-261-314	Sequence 314, App
30	26	18.4	25	8	US-08-809-423A-31	Sequence 31, Appl
31	26	18.4	25	9	US-09-864-761-45572	Sequence 45572, A
32	26	18.4	25	9	US-09-749-637A-322	Sequence 322, App
33	26	18.4	25	10	US-09-774-639-263	Sequence 263, App
34	26	18.4	25	10	US-09-569-730-362	Sequence 362, App
35	26	18.4	25	10	US-09-911-569-118	Sequence 118, App
36	26	18.4	25	13	US-10-067-422-28	Sequence 28, Appl
37	26	18.4	25	14	US-10-228-063-31	Sequence 31, Appl
38	26	18.4	25	14	US-10-200-879-118	Sequence 118, App
39	26	18.4	25	14	US-10-247-960-4	Sequence 4, Appl
40	26	18.4	25	14	US-10-271-344-31	Sequence 31, Appl
41	26	18.4	25	16	US-10-621-363-362	Sequence 362, App
42	25.5	18.1	25	9	US-09-973-451-26	Sequence 26, Appl
43	25.5	18.1	25	9	US-09-757-774-16	Sequence 16, Appl
44	25.5	18.1	25	14	US-10-059-261-313	Sequence 313, App
45	25	17.7	25	9	US-09-840-277-119	Sequence 119, App

ALIGNMENTS

RESULT 1

US-09-909-348-5
; Sequence 5, Application US/09909348
; Patent No. US20020042373A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; APPLICANT: Crowther, Roger S.
; APPLICANT: Stierberg, Janet
; APPLICANT: Bergmann, John
; TITLE OF INVENTION: Stimulation Of Cartilage Growth With Agonists
; TITLE OF INVENTION: Of The No. US20020042373A1-Proteolytically Activated Thrombin
; FILE REFERENCE: 3033.1003-001
; CURRENT APPLICATION NUMBER: US/09/909,348
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/219,800
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide fragment of Thrombin
US-09-909-348-5

Query Match 100.0%; Score 141; DB 9; Length 25;
Best Local Similarity 100.0%; Pred.No. 4.7e-12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTRYKPDGKRGDACEGDSGGPFV 25

DB 1 AGTRYKPDGKRGDACEGDSGGPFV 25

RESULT 2

US-09-909-122-5
; Sequence 5, Application US/09909122

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; Patent No. US20020128202A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; APPLICANT: Crowther, Roger S.
; APPLICANT: Simmons, David J.
; APPLICANT: Yang, Jiping
; APPLICANT: Redin, William R.
; TITLE OF INVENTION: Stimulation Of Bone Growth With Thrombin
; TITLE OF INVENTION: Peptide Derivatives
; FILE REFERENCE: 3033.1002-001
; CURRENT APPLICATION NUMBER: US/09/909,122
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/219,300
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide fragment of Thrombin
US-09-909-122-5

Query Match      100.0%; Score 141; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.7e-12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTRYKPDGKRGDACEGDSGGPFV 25
DB 1 AGTRYKPDGKRGDACEGDSGGPFV 25

RESULT 3
US-10-050-692-5
; Sequence 5, Application US/10050692
; Publication No. US20020182205A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; APPLICANT: Crowther, Roger S.
; APPLICANT: Simmons, David J.
; APPLICANT: Yang, Jiping
; APPLICANT: Redin, William R.
; TITLE OF INVENTION: STIMULATION OF BONE GROWTH WITH THROMBIN
; TITLE OF INVENTION: PEPTIDE DERIVATIVES
; FILE REFERENCE: 3033.1002-004
; CURRENT APPLICATION NUMBER: US/10/050,692
; CURRENT FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: 09/909,122
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/219,300
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fragment of human prothrombin
US-10-050-692-5

Query Match      100.0%; Score 141; DB 13; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.7e-12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTRYKPDGKRGDACEGDSGGPFV 25
DB 1 AGTRYKPDGKRGDACEGDSGGPFV 25

RESULT 4
US-10-353-522A-1
; Sequence 1, Application US/10353522A
; Publication No. US20030216296A1
; GENERAL INFORMATION:
; APPLICANT: WelGene Pharmaceuticals, Inc.
; APPLICANT: Park, Jong-Gu
; APPLICANT: Moon, Ik-Jae
; APPLICANT: Kim, Young-Cheol
; TITLE OF INVENTION: Peptide for Increasing Transfection Efficiency
; FILE REFERENCE: 57354-13USA
; CURRENT APPLICATION NUMBER: US/10/353,522A
; CURRENT FILING DATE: 2003-01-28
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 25
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: RGD-RGD-TatC-RGD-RGD
US-10-353-522A-1

Query Match      27.0%; Score 38; DB 15; Length 25;
Best Local Similarity 40.0%; Pred. No. 2.4e+02;
Matches 8; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

QY 2 GTRYKPDGKRGDACEGDSG 21
DB 5 GDRKKRRRRPPQCRGDRG 24

RESULT 5
US-09-864-761-37498
; Sequence 37498, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecm1ca-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/006666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006670
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; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: US 60/234,687
 ; PRIOR FILING DATE: 2000-09-21
 ; PRIOR APPLICATION NUMBER: US 09/608,408
 ; PRIOR FILING DATE: 2000-06-30
 ; PRIOR APPLICATION NUMBER: US 09/774,203
 ; PRIOR FILING DATE: 2001-01-29
 ; NUMBER OF SEQ ID NOS: 49117
 ; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
 ; SEQ ID NO 37498
 ; LENGTH: 25
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: MAP TO AC011504.2
 ; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 10
 ; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 9
 ; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 10
 ; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 8.6
 ; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 9.1
 ; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 11
 ; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 8.9
 ; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 10
 ; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 10
 ; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 9.5
 ; OTHER INFORMATION: SWISSPROT HIT: P22857, EVALUATION 1.70e+00
 US-09-864-761-37498

Query Match 25.5%; Score 36; DB 9; Length 25;
 Best Local Similarity 56.7%; Pred. No. 4.4e+02;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 15 ACBGDSGGP 23
 DB 11 ACQSRSGP 19

RESULT 6
 US-09-864-761-43492
 ; Sequence 43492, Application US/09864761
 ; Patent No. US2002048763A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Penn, Sharon G.
 ; APPLICANT: Rank, David R.
 ; APPLICANT: Hanzel, David K.
 ; APPLICANT: Chen, Wensheng
 ; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
 ; FILE REFERENCE: Reonica-X-1
 ; CURRENT APPLICATION NUMBER: US/09/864,761
 ; CURRENT FILING DATE: 2001-05-23
 ; PRIOR APPLICATION NUMBER: US 60/180,312
 ; PRIOR FILING DATE: 2000-02-04
 ; PRIOR APPLICATION NUMBER: US 60/207,456
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: US 09/632,366
 ; PRIOR FILING DATE: 2000-08-03
 ; PRIOR APPLICATION NUMBER: GB 24263.6
 ; PRIOR FILING DATE: 2000-10-04
 ; PRIOR APPLICATION NUMBER: US 60/236,359
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: PCT/US01/00666
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00667
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00664
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00669
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00665
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00668
 ; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00663
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00662
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00661
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00670
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: US 60/234,687
 ; PRIOR FILING DATE: 2000-09-21
 ; PRIOR APPLICATION NUMBER: US 09/608,408
 ; PRIOR FILING DATE: 2000-06-30
 ; PRIOR APPLICATION NUMBER: US 09/774,203
 ; PRIOR FILING DATE: 2001-01-29
 ; NUMBER OF SEQ ID NOS: 49117
 ; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
 ; SEQ ID NO 43492
 ; LENGTH: 25
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: MAP TO AC006324.2
 ; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.6
 ; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.72
 ; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.8
 ; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1
 ; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.75
 ; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.61
 US-09-864-761-43492

Query Match 23.4%; Score 33; DB 9; Length 25;
 Best Local Similarity 40.0%; Pred. No. 1.1e+03;
 Matches 6; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 8 DEGRKGDACGDSGG 22
 DB 10 EECMGDEPDHGG 24

RESULT 7
 US-10-280-066-233
 ; Sequence 233, Application US/10280066
 ; Publication No. US20030180718A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Pillutla, Renuka C.
 ; APPLICANT: Brissette, Renee
 ; APPLICANT: Spruyt, Michael
 ; APPLICANT: Dedova, Olga
 ; APPLICANT: Blume, Arthur J.
 ; APPLICANT: Prendergast, John
 ; APPLICANT: Goldstein, Neil I.
 ; TITLE OF INVENTION: TARGET SPECIFIC SCREENING AND ITS USE FOR IDENTIFYING TARGET BI
 ; FILE REFERENCE: 2598-4009US1
 ; CURRENT APPLICATION NUMBER: US/10/280,066
 ; CURRENT FILING DATE: 2002-10-24
 ; PRIOR APPLICATION NUMBER: 60/345,471
 ; PRIOR FILING DATE: 2001-10-24
 ; NUMBER OF SEQ ID NOS: 537
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 233
 ; LENGTH: 25
 ; TYPE: PRT
 ; ORGANISM: Escherichia coli
 ; FEATURE:
 ; NAME/KEY: MISC FEATURE
 ; OTHER INFORMATION: 07903-DG12-20M-PP-BC-C5
 US-10-280-066-233

Query Match 22.3%; Score 31.5; DB 14; Length 25;
 Best Local Similarity 52.9%; Pred. No. 1.7e+03;
 Matches 9; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY 1 AGTRYKPDGKRGDACE 17

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Db      10 AGFRLVRGAGDRGD-CE 25

Query Match      22.0%; Score 31; DB 10; Length 25;
Best Local Similarity 57.1%; Pred. No. 2e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      18 GDSGGPFV 24
        |:|:|:|:|:
Db      16 GEAGGPY 22

RESULT 8
US-09-852-455-75
; Sequence 75, Application US/09852455
; Publication No. US20030054348A1
; GENERAL INFORMATION:
; APPLICANT: BLUME ARTHUR J.
; APPLICANT: GOLDSTEIN, NEIL
; APPLICANT: PILLUTA, RENUKA
; APPLICANT: HSIAO, KU-CHUAN
; APPLICANT: PRENBERGAST, JOHN
; TITLE OF INVENTION: METHODS OF IDENTIFYING THE ACTIVITY OF GENE PRODUCTS
; FILE REFERENCE: 2598-4004US1
; CURRENT APPLICATION NUMBER: US/09/852,455
; CURRENT FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: 60/202,912
; PRIOR FILING DATE: 2000-05-09
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 75
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Homo sapiens
;
US-09-852-455-75

Query Match      22.0%; Score 31; DB 10; Length 25;
Best Local Similarity 75.0%; Pred. No. 2e+03;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      18 GDSGGPFV 25
        |:|:|:|:|:
Db      2 GDSGGALV 9

RESULT 9
US-09-962-756-1099
; Sequence 1099, Application US/09962756
; Publication No. US20030195147A1
; GENERAL INFORMATION:
; APPLICANT: PILLUTLA, RENUKA
; APPLICANT: BRISSETTE, RENEE
; APPLICANT: BLUME, ARTHUR J.
; APPLICANT: SCHAEFER, LAUGE
; APPLICANT: BRANDT, JAKOB
; APPLICANT: GOLDSTEIN, NEIL I.
; APPLICANT: SPETZLER, JANE
; APPLICANT: OSTERGAARD, SOREN
; APPLICANT: HANSEN, PER HERTZ
; TITLE OF INVENTION: INSULIN AND IGF-1 RECEPTOR AGONISTS AND ANTAGONISTS
; FILE REFERENCE: 1878-4051US1
; CURRENT APPLICATION NUMBER: US/09/962,756
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/538,038
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/146,127
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 1099
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
;
US-09-962-756-1099

Query Match      22.0%; Score 31; DB 14; Length 25;
Best Local Similarity 46.2%; Pred. No. 2e+03;
Matches 6; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY      10 GKRGDACEGDSGG 22
        |:|:|:|:|:
Db      7 GGGGGCGGGGGGG 19

RESULT 11
US-10-289-660-205
; Sequence 205, Application US/10289660
; Publication No. US20030157561A1
; GENERAL INFORMATION:
; APPLICANT: KOLKMAN, JOOST A.
; APPLICANT: STEMMER, WILLEM P.C.
; APPLICANT: GOVINDARAJAN, SRIDHAR
; TITLE OF INVENTION: COMBINATORIAL LIBRARIES OF MONOMER DOMAINS
; FILE REFERENCE: 0319.510US
; CURRENT APPLICATION NUMBER: US/10/289,660
; CURRENT FILING DATE: 2003-11-06
; PRIOR APPLICATION NUMBER: 10/133,128
;
US-10-289-660-205

Query Match      22.0%; Score 31; DB 10; Length 25;
Best Local Similarity 57.1%; Pred. No. 2e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      18 GDSGGPFV 24
        |:|:|:|:|:
Db      16 GEAGGPY 22

RESULT 10
US-10-133-128-205
; Sequence 205, Application US/10133128
; Publication No. US20030082630A1
; GENERAL INFORMATION:
; APPLICANT: KOLKMAN, JOOST A.
; APPLICANT: STEMMER, WILLEM P.C.
; TITLE OF INVENTION: COMBINATORIAL LIBRARIES OF MONOMER DOMAINS
; FILE REFERENCE: 0319.410US
; CURRENT APPLICATION NUMBER: US/10/133,128
; CURRENT FILING DATE: 2002-04-26
; PRIOR APPLICATION NUMBER: 60/374,107
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: 60/333,359
; PRIOR FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 60/337,209
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/286,823
; PRIOR FILING DATE: 2001-04-26
; NUMBER OF SEQ ID NOS: 244
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 205
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide linker
;
US-10-133-128-205

Query Match      22.0%; Score 31; DB 10; Length 25;
Best Local Similarity 46.2%; Pred. No. 2e+03;
Matches 6; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY      10 GKRGDACEGDSGG 22
        |:|:|:|:|:
Db      7 GGGGGCGGGGGGG 19

RESULT 11
US-10-289-660-205
; Sequence 205, Application US/10289660
; Publication No. US20030157561A1
; GENERAL INFORMATION:
; APPLICANT: KOLKMAN, JOOST A.
; APPLICANT: STEMMER, WILLEM P.C.
; APPLICANT: GOVINDARAJAN, SRIDHAR
; TITLE OF INVENTION: COMBINATORIAL LIBRARIES OF MONOMER DOMAINS
; FILE REFERENCE: 0319.510US
; CURRENT APPLICATION NUMBER: US/10/289,660
; CURRENT FILING DATE: 2003-11-06
; PRIOR APPLICATION NUMBER: 10/133,128
;
US-10-289-660-205
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; PRIOR FILING DATE: 2002-04-26
 ; PRIOR APPLICATION NUMBER: 60/374,107
 ; PRIOR FILING DATE: 2002-04-18
 ; PRIOR APPLICATION NUMBER: 60/333,359
 ; PRIOR FILING DATE: 2001-11-26
 ; PRIOR APPLICATION NUMBER: 60/337,209
 ; PRIOR FILING DATE: 2001-11-19
 ; PRIOR APPLICATION NUMBER: 60/286,823
 ; PRIOR FILING DATE: 2001-04-26
 ; NUMBER OF SEQ ID NOS: 24
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 205
 ; LENGTH: 25
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 ; OTHER INFORMATION: peptide linker
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)..(12)
 ; OTHER INFORMATION: This region may vary in length from 1-12 residues,
 ; OTHER INFORMATION: 3-9 residues, 4-8 residues or 4-7 residues
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (14)..(25)
 ; OTHER INFORMATION: This region may vary in length from 1-12 residues,
 ; OTHER INFORMATION: 3-9 residues, 4-8 residues or 4-7 residues
 ; US-10-289-660-205

Query Match 22.0%; Score 31; DB 14; Length 25;
 Best Local Similarity 46.2%; Pred. No. 2e+03;
 Matches 6; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 10 GKGACAGDSCG 22
 DB 7 GGGGGGGGGGG 19

RESULT 12
 US-10-253-471-1099
 ; Sequence 1099, Application US/10253471
 ; Publication No. US20030236190A1
 ; GENERAL INFORMATION:
 ; APPLICANT: PILLUTLA, RENUKA et al.
 ; TITLE OF INVENTION: INSULIN AND IGF-1 RECEPTOR AGONISTS AND ANTAGONISTS
 ; FILE REFERENCE: 1878-4057
 ; CURRENT APPLICATION NUMBER: US/10/253,471
 ; CURRENT FILING DATE: 2002-09-24
 ; PRIOR APPLICATION NUMBER: 09/962,756
 ; PRIOR FILING DATE: 2001-09-24
 ; PRIOR APPLICATION NUMBER: 09/538,038
 ; PRIOR FILING DATE: 2000-03-29
 ; PRIOR APPLICATION NUMBER: 09/146,127
 ; PRIOR FILING DATE: 1998-09-02
 ; NUMBER OF SEQ ID NOS: 227
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1099
 ; LENGTH: 25
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 ; OTHER INFORMATION: peptide
 ; FEATURE:
 ; NAME/KEY: MOD_RES
 ; LOCATION: (13)
 ; OTHER INFORMATION: Unknown amino acid; translation read-through at
 ; OTHER INFORMATION: TGA stop codon
 ; US-10-253-471-1099

Query Match 22.0%; Score 31; DB 15; Length 25;
 Best Local Similarity 57.1%; Pred. No. 2e+03;

Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 18 GDSGGPF 24
 DB 16 GRAGGPY 22

RESULT 13
 US-10-253-493-1099
 ; Sequence 1099, Application US/10253493
 ; Publication No. US20040023887A1
 ; GENERAL INFORMATION:
 ; APPLICANT: PILLUTLA, RENUKA et al.
 ; TITLE OF INVENTION: INSULIN AND IGF-1 RECEPTOR AGONISTS AND ANTAGONISTS
 ; FILE REFERENCE: 1878-4056
 ; CURRENT APPLICATION NUMBER: US/10/253,493
 ; CURRENT FILING DATE: 2002-09-24
 ; PRIOR APPLICATION NUMBER: 09/962,756
 ; PRIOR FILING DATE: 2001-09-24
 ; PRIOR APPLICATION NUMBER: 09/538,038
 ; PRIOR FILING DATE: 2000-03-29
 ; PRIOR APPLICATION NUMBER: 09/146,127
 ; PRIOR FILING DATE: 1998-09-02
 ; NUMBER OF SEQ ID NOS: 227
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1099
 ; LENGTH: 25
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 ; OTHER INFORMATION: peptide
 ; FEATURE:
 ; NAME/KEY: MOD_RES
 ; LOCATION: (13)
 ; OTHER INFORMATION: Unknown amino acid; translation read-through at
 ; OTHER INFORMATION: TGA stop codon
 ; US-10-253-493-1099

Query Match 22.0%; Score 31; DB 16; Length 25;
 Best Local Similarity 57.1%; Pred. No. 2e+03;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 18 GDSGGPF 24
 DB 16 GRAGGPY 22

RESULT 14
 US-09-933-767-598
 ; Sequence 598, Application US/09933767
 ; Publication No. US20030181692A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ni et al.
 ; TITLE OF INVENTION: 207 Human Secreted Proteins
 ; FILE REFERENCE: E2007P2
 ; CURRENT APPLICATION NUMBER: US/09/933,767
 ; CURRENT FILING DATE: 2001-08-22
 ; PRIOR APPLICATION NUMBER: PCT/US01/05614
 ; PRIOR FILING DATE: 2001-02-21
 ; PRIOR APPLICATION NUMBER: 60/184,836
 ; PRIOR FILING DATE: 2000-02-24
 ; PRIOR APPLICATION NUMBER: 60/193,170
 ; PRIOR FILING DATE: 2000-03-29
 ; PRIOR APPLICATION NUMBER: 09/205,258
 ; PRIOR FILING DATE: 1998-12-04
 ; PRIOR APPLICATION NUMBER: PCT/US98/11422
 ; PRIOR FILING DATE: 1998-06-04
 ; PRIOR APPLICATION NUMBER: 60/048,885
 ; PRIOR FILING DATE: 1997-06-06
 ; PRIOR APPLICATION NUMBER: 60/049,375
 ; PRIOR FILING DATE: 1997-06-06
 ; PRIOR APPLICATION NUMBER: 60/048,881

1 PRIOR FILING DATE: 1997-06-06
2 PRIOR APPLICATION NUMBER: 60/048,880
3 PRIOR FILING DATE: 1997-06-06
4 PRIOR APPLICATION NUMBER: 60/048,896
5 PRIOR FILING DATE: 1997-06-06
6 PRIOR APPLICATION NUMBER: 60/049,020
7 PRIOR FILING DATE: 1997-06-06
8 PRIOR APPLICATION NUMBER: 60/048,876
9 PRIOR FILING DATE: 1997-06-06
10 PRIOR APPLICATION NUMBER: 60/048,895
11 PRIOR FILING DATE: 1997-06-06
12 PRIOR APPLICATION NUMBER: 60/048,884
13 PRIOR FILING DATE: 1997-06-06
14 PRIOR APPLICATION NUMBER: 60/048,894
15 PRIOR FILING DATE: 1997-06-06
16 PRIOR APPLICATION NUMBER: 60/048,971
17 PRIOR FILING DATE: 1997-06-06
18 PRIOR APPLICATION NUMBER: 60/048,964
19 PRIOR FILING DATE: 1997-06-06
20 PRIOR APPLICATION NUMBER: 60/048,882
21 PRIOR FILING DATE: 1997-06-06
22 PRIOR APPLICATION NUMBER: 60/048,899
23 PRIOR FILING DATE: 1997-06-06
24 PRIOR APPLICATION NUMBER: 60/048,893
25 PRIOR FILING DATE: 1997-06-06
26 PRIOR APPLICATION NUMBER: 60/048,900
27 PRIOR FILING DATE: 1997-06-06
28 PRIOR APPLICATION NUMBER: 60/048,901
29 PRIOR FILING DATE: 1997-06-06
30 PRIOR APPLICATION NUMBER: 60/048,892
31 PRIOR FILING DATE: 1997-06-06
32 PRIOR APPLICATION NUMBER: 60/048,915
33 PRIOR FILING DATE: 1997-06-06
34 PRIOR APPLICATION NUMBER: 60/049,019
35 PRIOR FILING DATE: 1997-06-06
36 PRIOR APPLICATION NUMBER: 60/048,970
37 PRIOR FILING DATE: 1997-06-06
38 PRIOR APPLICATION NUMBER: 60/048,972
39 PRIOR FILING DATE: 1997-06-06
40 PRIOR APPLICATION NUMBER: 60/048,916
41 PRIOR FILING DATE: 1997-06-06
42 PRIOR APPLICATION NUMBER: 60/049,373
43 PRIOR FILING DATE: 1997-06-06
44 PRIOR APPLICATION NUMBER: 60/048,875
45 PRIOR FILING DATE: 1997-06-06
46 PRIOR APPLICATION NUMBER: 60/049,374
47 PRIOR FILING DATE: 1997-06-06
48 PRIOR APPLICATION NUMBER: 60/048,917
49 PRIOR FILING DATE: 1997-06-06
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52 PRIOR APPLICATION NUMBER: 60/048,974
53 PRIOR FILING DATE: 1997-06-06
54 PRIOR APPLICATION NUMBER: 60/048,883
55 PRIOR FILING DATE: 1997-06-06
56 PRIOR APPLICATION NUMBER: 60/048,897
57 PRIOR FILING DATE: 1997-06-06
58 PRIOR APPLICATION NUMBER: 60/048,898
59 PRIOR FILING DATE: 1997-06-06
60 PRIOR APPLICATION NUMBER: 60/048,962
61 PRIOR FILING DATE: 1997-06-06
62 PRIOR APPLICATION NUMBER: 60/048,963
63 PRIOR FILING DATE: 1997-06-06
64 PRIOR APPLICATION NUMBER: 60/048,877
65 PRIOR FILING DATE: 1997-06-06
66 PRIOR APPLICATION NUMBER: 60/048,878
67 PRIOR FILING DATE: 1997-06-06
68 PRIOR APPLICATION NUMBER: 60/068,054
69 PRIOR FILING DATE: 1997-12-18
70 PRIOR APPLICATION NUMBER: 60/068,064
71 PRIOR FILING DATE: 1997-12-18
72 PRIOR APPLICATION NUMBER: 60/068,053
73 PRIOR FILING DATE: 1997-12-18

1 PRIOR APPLICATION NUMBER: 60/070,923
2 PRIOR FILING DATE: 1997-12-18
3 PRIOR APPLICATION NUMBER: 60/073,160
4 PRIOR FILING DATE: 1998-01-30
5 PRIOR APPLICATION NUMBER: 60/073,159
6 PRIOR FILING DATE: 1998-01-30
7 PRIOR APPLICATION NUMBER: 60/073,165
8 PRIOR FILING DATE: 1998-01-30
9 PRIOR APPLICATION NUMBER: 60/073,164
10 PRIOR FILING DATE: 1998-01-30
11 PRIOR APPLICATION NUMBER: 60/085,925
12 PRIOR FILING DATE: 1998-05-18
13 PRIOR APPLICATION NUMBER: 60/085,921
14 PRIOR FILING DATE: 1998-05-18
15 PRIOR APPLICATION NUMBER: 60/085,923
16 PRIOR FILING DATE: 1998-05-18
17 PRIOR APPLICATION NUMBER: 60/085,922
18 PRIOR FILING DATE: 1998-05-18
19 PRIOR APPLICATION NUMBER: 60/092,921
20 PRIOR FILING DATE: 1998-07-15
21 PRIOR APPLICATION NUMBER: 60/094,657
22 PRIOR FILING DATE: 1998-07-30
23 NUMBER OF SEQ ID NOS: 1245
24 SOFTWARE: PatentIn Ver. 2.0
25 SEQ ID NO 598
26 LENGTH: 25
27 TYPE: PRT
28 ORGANISM: Homo sapiens
29 US-09-933-767-598
30
31 Query Match 21.3%; Score 30; DB 10; Length 25;
32 Best Local Similarity 42.9%; Pred. No. 2.8e+03;
33 Matches 6; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
34
35 Qy 9 EGKGDACGDSGG 22
36 |||: ||: : |
37 Db 4 EGKGRKACNCTCG 17
38
39 RESULT 15
40 US-10-036-869-7
41 Sequence 7, Application US/10036869
42 Publication No. US20020151516A1
43 GENERAL INFORMATION:
44 APPLICANT: Mixson, James A
45 TITLE OF INVENTION: CARRIER-DNA COMPLEXES CONTAINING DNA
46 ENCODING ANTI-ANGIOGENIC PEPTIDES AND THEIR USE IN GENE
47 THERAPY
48
49 NUMBER OF SEQUENCES: 43
50 CORRESPONDENCE ADDRESS:
51 ADDRESSEE: Connolly, Bove, Lodge, & Hutz
52 STREET: 1220 Market Street, P.O. Box 2207
53 CITY: Wilmington
54 STATE: Delaware
55 COUNTRY: U.S.A.
56 ZIP: 19899
57 COMPUTER READABLE FORM:
58 MEDIUM TYPE: Floppy disk
59 COMPUTER: IBM PC compatible
60 OPERATING SYSTEM: PC-DOS/MS-DOS
61 SOFTWARE: PatentIn Release #1.0, Version #1.25
62 CURRENT APPLICATION DATA:
63 APPLICATION NUMBER: US/10/036,869
64 FILING DATE: 29-Nov-02 US20020151516A1-2001
65 CLASSIFICATION: <Unknown>
66 PRIOR APPLICATION DATA:
67 APPLICATION NUMBER: US/08/985,526
68 FILING DATE: <Unknown>
69 APPLICATION NUMBER: US 08/608,845
70 FILING DATE: 16-JUL-1996
71 ATTORNEY/AGENT INFORMATION:
72 NAME: McMorris Jr., Robert G
73 TELECOMMUNICATION INFORMATION:

/ TELEPHONE: (302) 658-9141
 / TELEFAX: (302) 658-5613
 / INFORMATION FOR SEQ ID NO: 7:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 25 amino acids
 / TYPE: amino acid
 / TOPOLOGY: linear
 / SEQUENCE DESCRIPTION: SEQ ID NO: 7:
 US-10-036-869-7

Query Match 21.3%; Score 30; DB 13; Length 25;
 Best Local Similarity 40.0%; Pred. No. 2.8e-03;
 Matches 8; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

QY 2 GTRYKPDGKRGDACEGDSG 21
 | | | | | | | | | |
 Db 4 GSRGKSYIGSRGKSYIGSRG 23

Search completed: February 26, 2004, 09:54:54
 Job time : 35 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 26, 2004, 09:47:18 ; Search time 23 Seconds
(without alignments)
56.115 Million cell updates/sec

Title: US-09-909-348-5

Perfect score: 141

Sequence: 1 AGTRYKPDGKRGDACEGDSGPFV 25

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 2669

Minimum DB seq length: 25

Maximum DB seq length: 25

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*

1: /cgn2_6/ptodata/2/iaa/5A-COMB.pep.*

2: /cgn2_6/ptodata/2/iaa/5B-COMB.pep.*

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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	21.3	25	3	US-08-985-526-7
2	30	21.3	25	4	US-08-900-230-29
3	30	21.3	25	4	US-09-205-258-598
4	29	20.6	25	2	US-08-473-475A-7
5	29	20.6	25	2	US-08-263-911-5
6	29	20.6	25	3	US-09-184-658-42
7	29	20.6	25	3	US-08-463-903-31
8	29	20.6	25	3	US-08-454-098-24
9	29	20.6	25	3	US-08-975-084-2
10	29	20.6	25	4	US-07-935-695-31
11	29	20.6	25	4	US-09-504-262D-42
12	27.5	19.5	25	1	US-08-502-989-1
13	27.5	19.5	25	1	US-08-502-989-12
14	27.5	19.5	25	1	US-08-502-989-13
15	27.5	19.5	25	1	US-08-502-989-20
16	27.5	19.5	25	1	US-08-502-989-21
17	27.5	19.5	25	1	US-08-502-989-22
18	27.5	19.5	25	4	US-09-381-009-23
19	27.5	19.5	25	5	PCT-US94-05355-1
20	27.5	19.5	25	5	PCT-US94-05355-12
21	27.5	19.5	25	5	PCT-US94-05355-13
22	27.5	19.5	25	5	PCT-US94-05355-20
23	27.5	19.5	25	5	PCT-US94-05355-21
24	27.5	19.5	25	5	PCT-US94-05355-22
25	27	19.1	25	1	US-08-457-229-3
26	27	19.1	25	2	US-08-457-487-3
27	27	19.1	25	2	US-08-404-531B-39

28	27	19.1	25	2	US-08-479-733A-32	Sequence 32, Appl
29	27	19.1	25	2	US-08-350-212-3	Sequence 3, Appl
30	27	19.1	25	3	US-08-476-900A-39	Sequence 39, Appl
31	27	19.1	25	3	US-08-479-737A-32	Sequence 32, Appl
32	27	19.1	25	3	US-08-488-546A-39	Sequence 39, Appl
33	27	19.1	25	3	US-08-482-369A-32	Sequence 32, Appl
34	27	19.1	25	3	US-09-207-277-3	Sequence 3, Appl
35	27	19.1	25	4	US-09-357-592-3	Sequence 3, Appl
36	27	19.1	25	5	PCT-US93-01652-2	Sequence 11, Appl
37	26.5	18.8	25	1	US-08-502-989-11	Sequence 11, Appl
38	26.5	18.8	25	5	PCT-US94-05355-11	Sequence 11, Appl
39	26	18.4	25	1	US-08-383-348A-10	Sequence 10, Appl
40	26	18.4	25	1	US-08-383-804B-10	Sequence 10, Appl
41	26	18.4	25	1	US-08-383-748A-10	Sequence 10, Appl
42	26	18.4	25	1	US-08-446-652-82	Sequence 82, Appl
43	26	18.4	25	1	US-08-487-001A-31	Sequence 31, Appl
44	26	18.4	25	1	US-08-814-309A-10	Sequence 10, Appl
45	26	18.4	25	2	US-08-630-822A-31	Sequence 31, Appl

ALIGNMENTS

RESULT 1
US-08-985-526-7
; Sequence 7, Application US/08985526
; Patent No. 6080728
; GENERAL INFORMATION:
; APPLICANT: Mixson, James A
; TITLE OF INVENTION: CARRIER:DNA COMPLEXES CONTAINING DNA
; TITLE OF INVENTION: ENCODING ANTI-ANGIOGENIC PEPTIDES AND THEIR USE IN GENE
; TITLE OF INVENTION: THERAPY
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Connolly, Bove, Lodge, & Hutz
; STREET: 1220 Market Street, P.O. Box 2207
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: U.S.A.
; ZIP: 19899
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,526
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA: US 08/508,845
; FILING DATE: 16-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: McMorro Jr., Robert G
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302) 658-9141
; TELEFAX: (302) 658-5613
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-985-526-7

Query Match 21.3%; Score 30; DB 3; Length 25;
Best Local Similarity 40.0%; Pred. No. 8.2e+02;
Matches 8; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

QY 2 GTRYKPDGKRGDACEGDSG 21

Db 4 GSRGKSVIGSRGKSVIGSRG 23

RESULT 2

US-08-900-230-29
; Sequence 29, Application US/08900230
; Patent No. 6329197
; GENERAL INFORMATION:
; APPLICANT: Bard, Jonathan A.
; TITLE OF INVENTION: DNA ENCODING GALANN GALR3 RECEPTORS AND
; TITLE OF INVENTION: USES THEREOF
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of The Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 11036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/900,230
; FILING DATE: 23-JUL-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 52241-C/JPW/ADM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE:
; HYPOTHEetical: NO
; ANTI-SENSE: NO
US-08-900-230-29

Query Match 21.3%; Score 30; DB 4; Length 25;
Best Local Similarity 46.2%; Pred. No. 8.2e+02;
Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 10 GKRGDACGDSGG 22
DB 5 GCAGAACTGGTAG 17

RESULT 3

US-09-205-258-598
; Sequence 598, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896

; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,882
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,899
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,893
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,915
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,019
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,972
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,916
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,373
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,875
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,374
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,917
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,949
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,883
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,897
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,898
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,962
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 598
; LENGTH: 25

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-205-258-598

Query Match      21.3%  Score 30;  DB 4;  Length 25;
Best Local Similarity 42.9%  Pred. No. 8.2e+02;
Matches 6;  Conservative 3;  Mismatches 5;  Indels 0;  Gaps 0;

QY  9  EGKRGDACEGDSG 22
Db   4  EGKRRACKNCTCG 17

RESULT 4
US-08-473-475A-7
; Sequence 7, Application US/08473475A
; Patent No. 5843450
; GENERAL INFORMATION:
; APPLICANT: DAWSON, GEORGE
; APPLICANT: BRIDON, DOMINIQUE P.
; APPLICANT: SCHROEDER-POJIAK, PAMELLA A.
; APPLICANT: KNIGGE, MARK P.
; APPLICANT: JARFE, KEVE
; TITLE OF INVENTION: HEPATITIS GB VIRUS SYNTHETIC PEPTIDES
; TITLE OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/473,475A
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: FOREMSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33206
; REFERENCE/DOCKET NUMBER: 5547US.P8
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-937-2623
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-473-475A-7

Query Match      20.6%  Score 29;  DB 2;  Length 25;
Best Local Similarity 42.9%  Pred. No. 1.1e+03;
Matches 5;  Conservative 2;  Mismatches 6;  Indels 0;  Gaps 0;

QY  7  PDEGKRGDACEGDS 20
Db   10  PESLQRSDPLEGPS 23

RESULT 5
US-08-263-911-5
; Sequence 5, Application US/08263911
; Patent No. 5877291
; GENERAL INFORMATION:
; APPLICANT: Mezes, Peter S
```

```
; APPLICANT: Gourlie, Brian B
; TITLE OF INVENTION: MULTIVALENT SINGLE CHAIN ANTIBODIES
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Duane C. Ulmer
; STREET: P.O. Box 1967
; CITY: Midland
; STATE: MI
; COUNTRY: US
; ZIP: 48641-1967
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/263,911
; FILING DATE: 21-JUN-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/990,263
; FILING DATE: 11-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Ulmer, Duane C
; REGISTRATION NUMBER: 34,941
; REFERENCE/DOCKET NUMBER: C-41,014
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (517) 636-8104
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-263-911-5

Query Match      20.6%  Score 29;  DB 2;  Length 25;
Best Local Similarity 40.0%  Pred. No. 1.1e+03;
Matches 6;  Conservative 3;  Mismatches 6;  Indels 0;  Gaps 0;

QY  6  KPDEGKRGDACEGDS 20
Db   7  KKDAAKDDAKKDDA 21

RESULT 6
US-09-184-658-42
; Sequence 42, Application US/09184658
; Patent No. 6030792
; GENERAL INFORMATION:
; APPLICANT: Otterness, Ivan G.
; APPLICANT: Mezes, Peter S.
; APPLICANT: Downs, James T.
; APPLICANT: Johnson, Kimberly S.
; TITLE OF INVENTION: Assays for Measurement of Protein Fragments in
; TITLE OF INVENTION: Biological Media
; FILE REFERENCE: PC9946-A
; CURRENT APPLICATION NUMBER: US/09/184,658
; CURRENT FILING DATE: 1998-11-02
; EARLIER APPLICATION NUMBER: 60/065,423
; EARLIER FILING DATE: 1997-11-13
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Single chain
; OTHER INFORMATION: antibody linker sequence.
US-09-184-658-42

Query Match      20.6%  Score 29;  DB 3;  Length 25;
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Best Local Similarity 40.0%; Pred. No. 1.1e+03;
Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 6 KPDEGKRGDACEGDS 20
Db 7 KDAAKKDDAKKDDA 21

RESULT 7

US-08-463-903-31
; Sequence 31, Application US/08463903
; Patent No. 6071515
; GENERAL INFORMATION:
; APPLICANT: Mezes, Peter S.
; APPLICANT: Richard, Ruth A.
; APPLICANT: Affholter, Joseph A.
; APPLICANT: Kotite, Nicolas J.
; TITLE OF INVENTION: Dimer and Multimer Forms of Single Chain Polypeptides
; FILE REFERENCE: 40224A US
; CURRENT APPLICATION NUMBER: US/08/463,903
; CURRENT FILING DATE: 1995-06-05
; EARLIER APPLICATION NUMBER: US 07/935,695
; EARLIER FILING DATE: 1992-08-21
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: MS-Word for Windows, Ver. 7.0
; SEQ ID NO 31
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: UNIHOPF linker
; LOCATION: 1..25
US-08-463-903-31

Query Match 20.6%; Score 29; DB 3; Length 25;
Best Local Similarity 40.0%; Pred. No. 1.1e+03;
Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 6 KPDEGKRGDACEGDS 20
Db 7 KDAAKKDDAKKDDA 21

RESULT 8

US-08-454-098-24
; Sequence 24, Application US/08454098
; Patent No. 6103521
; GENERAL INFORMATION:
; APPLICANT: CAPON, DANIEL J
; APPLICANT: SMITH, DOUGLAS H
; APPLICANT: TIAN, HUAN
; APPLICANT: WINSLOW, GENINE A
; APPLICANT: SIEKEVITZ, MIRIAM
; TITLE OF INVENTION: MULTISPECIFIC CHIMERIC RECEPTORS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CELL GENESYS, INC.
; STREET: 322 LAKESIDE DRIVE
; CITY: FOSTER CITY
; STATE: CALIFORNIA
; COUNTRY: US
; ZIP: 94404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/454,098
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/384,033

; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: KRUPEN, KAREN I
; REGISTRATION NUMBER: 34,647
; REFERENCE/DOCKET NUMBER: CELL 18
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 358-9600 x131
; TELEFAX: (415) 349-7392
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-454-098-24

Query Match 20.6%; Score 29; DB 3; Length 25;
Best Local Similarity 40.0%; Pred. No. 1.1e+03;
Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 6 KPDEGKRGDACEGDS 20
Db 7 KDAAKKDDAKKDDA 21

RESULT 9

US-08-975-084-2
; Sequence 2, Application US/08975084
; Patent No. 6258780
; GENERAL INFORMATION:
; APPLICANT: SOREQ, Hermona
; APPLICANT: FRIEDMAN, Alon
; APPLICANT: SEIDMAN, Shlomo
; APPLICANT: KAUFER, Daniela
; TITLE OF INVENTION: A METHOD AND COMPOSITION FOR ENABLING
; TITLE OF INVENTION: PASSAGE THROUGH THE BLOOD-BRAIN-BARRIER
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kohn & Associates
; STREET: 30500 No. 6258780thwestern Hwy., Suite 410
; CITY: Farmington Hills
; STATE: Michigan
; COUNTRY: US
; ZIP: 48334
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/975,084
; FILING DATE: 11-NOV-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Montgomery, Ilene N.
; REGISTRATION NUMBER: 38,972
; REFERENCE/DOCKET NUMBER: 2391.00082
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (248) 539-5050
; TELEFAX: (248) 539-5055
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-975-084-2

Query Match 20.6%; Score 29; DB 3; Length 25;
Best Local Similarity 40.0%; Pred. No. 1.1e+03;
Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Query Match

Best Local Similarity 40.0%; Pred. No. 1.1e+03;
Matches 6; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 9 EKRGDACEGSGP 23
Db 3 QPAGSGWEGSGSP 17

RESULT 10
US-07-935-695-31
; Sequence 31, Application US/07935695
; Patent No. 6329507
; GENERAL INFORMATION:
; APPLICANT: Mezes, Peter S.
; APPLICANT: Richard, Ruth A.
; APPLICANT: Affholter, Joseph A.
; APPLICANT: Kotite, Nicolas J.
; TITLE OF INVENTION: Dimer and Multimer Forms of Single Chain Polypeptides
; FILE REFERENCE: 40224A US
; CURRENT APPLICATION NUMBER: US/07/935,695
; CURRENT FILING DATE: 1992-08-21
; PRIOR APPLICATION NUMBER: US 08/463,903
; PRIOR FILING DATE: 1995-06-05
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: MS-Word for Windows, Ver. 7.0
; SEQ ID NO 31
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: UNIHOPe linker
; LOCATION: 1..25
; OTHER INFORMATION: ;
US-07-935-695-31

Query Match 20.6%; Score 29; DB 4; Length 25;
Best Local Similarity 40.0%; Pred. No. 1.1e+03;
Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 6 KPDEGKRGDACEGDS 20
Db 7 KXDAKKDDAKKDDA 21

RESULT 11
US-09-504-262D-42
; Sequence 42, Application US/09504262D
; Patent No. 6842007
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: Saltarelli, Mary J.
; APPLICANT: Johnson, Kimberly S.
; APPLICANT: Ottewill, Ivan G.
; TITLE OF INVENTION: Assays for Measurement of Type II Collagen Fragments in Urine
; FILE REFERENCE: PC10189GPR - CIP of PC9346A
; CURRENT APPLICATION NUMBER: US/09/504,262D
; CURRENT FILING DATE: 2000-02-15
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 42
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer for PCR-SOE
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Description of Artificial Sequence: Single chain antibody linker
; OTHER INFORMATION: sequence.
US-09-504-262D-42

Query Match 20.6%; Score 29; DB 4; Length 25;
Best Local Similarity 40.0%; Pred. No. 1.1e+03;

Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 6 KPDEGKRGDACEGDS 20
Db 7 KXDAKKDDAKKDDA 21

RESULT 12
US-08-502-989-1
; Sequence 1, Application US/08502989
; Patent No. 5681925
; GENERAL INFORMATION:
; APPLICANT: Broersma, Robert J
; APPLICANT: Cwen, Thomas J
; APPLICANT: Kristenansky, John L
; TITLE OF INVENTION: TRIFUNCTIONAL ANTI-THROMBIN AND
; TITLE OF INVENTION: ANTI-PLATELET PEPTIDES
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merrell Dow Pharmaceuticals Inc.
; STREET: 2110 E. Galbraith Road, P.O. Box 156300
; CITY: Cincinnati
; STATE: Ohio
; COUNTRY: USA
; ZIP: 45215-6300
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/502,989
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/076,066
; FILING DATE: 11-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Boudreaux, William R
; REGISTRATION NUMBER: 35,796
; REFERENCE/DOCKET NUMBER: M01696 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 513/948-6566
; TELEFAX: 513/948-7961 or 4681
; TELEX: 214320
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "Xaa at location 1 is
; OTHER INFORMATION: phenylalanine in the D-configuration"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 6
; OTHER INFORMATION: /note= "Xaa at location 6 is D-Cys
; OTHER INFORMATION: and is sulfide bonded to D-Cys at location 13"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 11
; OTHER INFORMATION: /note= "Xaa at location 11 is
; OTHER INFORMATION: norleucine"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 13
; OTHER INFORMATION: /note= "Xaa at location 13 is D-Cys
; OTHER INFORMATION: and is sulfide bonded to D-Cys at location 6"
; FEATURE:
; NAME/KEY: Modified-site

LOCATION: 24
OTHER INFORMATION: /note= "Xaa at location 24 is
FEATURE: cyclohexylalanine"
NAME/KEY: Modified-site
LOCATION: 25
OTHER INFORMATION: /note= "Xaa at location 25 is
OTHER INFORMATION: glutamic acid in the D-configuration"
US-08-502-989-1

Query Match 19.5%; Score 27.5; DB 1; Length 25;
Best Local Similarity 50.0%; Pred. No. 1.9e+03;
Matches 7; Conservative 1; Mismatches 5; Indels 1; Gaps 1;

QY 6 KPDEGKRGDACEGD 19
DB 3 RFGXG-RGDXPXGD 15

RESULT 13
US-08-502-989-12
Sequence 12, Application US/08502989
Patent No. 5681925
GENERAL INFORMATION:
APPLICANT: Broersma, Robert J
APPLICANT: Owen, Thomas J
TITLE OF INVENTION: TRIFUNCTIONAL ANTITHROMBIN AND
TITLE OF INVENTION: ANTIPLATELET PEPTIDES
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merrell Dow Pharmaceuticals Inc.
STREET: 2110 E. Galbraith Road, P.O. Box 156300
CITY: Cincinnati
STATE: Ohio
COUNTRY: USA
ZIP: 45215-6300
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/502,989
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/076,066
FILING DATE: 11-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Boudreaux, William R
REGISTRATION NUMBER: 35,796
REFERENCE/DOCKET NUMBER: M01696 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 513/948-6566
TELEFAX: 513/948-7961 or 4681
TELEX: 214320
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /note= "Xaa at location 1 is
OTHER INFORMATION: phenylalanine in the D-configuration"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 6
OTHER INFORMATION: /note= "Xaa at location 6 is D-Cys
OTHER INFORMATION: and is sulfide bonded to D-Cys at location 13"

FEATURE:
NAME/KEY: Modified-site
LOCATION: 11
OTHER INFORMATION: /note= "Xaa at location 11 is
OTHER INFORMATION: cyclohexylalanine"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 13
OTHER INFORMATION: /note= "Xaa at location 13 is D-Cys
OTHER INFORMATION: and is sulfide bonded to D-Cys at location 6"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 24
OTHER INFORMATION: /note= "Xaa at location 24 is
OTHER INFORMATION: cyclohexylalanine"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 25
OTHER INFORMATION: /note= "Xaa at location 25 is
OTHER INFORMATION: glutamic acid in the D-configuration"
US-08-502-989-12

Query Match 19.5%; Score 27.5; DB 1; Length 25;
Best Local Similarity 50.0%; Pred. No. 1.9e+03;
Matches 7; Conservative 1; Mismatches 5; Indels 1; Gaps 1;

QY 6 KPDEGKRGDACEGD 19
DB 3 RFGXG-RGDXPXGD 15

RESULT 14
US-08-502-989-13
Sequence 13, Application US/08502989
Patent No. 5681925
GENERAL INFORMATION:
APPLICANT: Broersma, Robert J
APPLICANT: Owen, Thomas J
APPLICANT: Krstenansky, John L
TITLE OF INVENTION: TRIFUNCTIONAL ANTITHROMBIN AND
TITLE OF INVENTION: ANTIPLATELET PEPTIDES
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merrell Dow Pharmaceuticals Inc.
STREET: 2110 E. Galbraith Road, P.O. Box 156300
CITY: Cincinnati
STATE: Ohio
COUNTRY: USA
ZIP: 45215-6300
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/502,989
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/076,066
FILING DATE: 11-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Boudreaux, William R
REGISTRATION NUMBER: 35,796
REFERENCE/DOCKET NUMBER: M01696 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 513/948-6566
TELEFAX: 513/948-7961 or 4681
TELEX: 214320
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acid

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; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "Xaa at location 1 is
; OTHER INFORMATION: phenylalanine in the D-configuration"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 6
; OTHER INFORMATION: /note= "Xaa at location 6 is
; OTHER INFORMATION: cysteine in the D-configuration"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 11
; OTHER INFORMATION: /note= "Xaa at location 11 is
; OTHER INFORMATION: norleucine"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 13
; OTHER INFORMATION: /note= "Xaa at location 13 is
; OTHER INFORMATION: penicillamine in the D-configuration"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 24
; OTHER INFORMATION: /note= "Xaa at location 24 is
; OTHER INFORMATION: cyclohexylalanine"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 25
; OTHER INFORMATION: /note= "Xaa at location 25 is
; OTHER INFORMATION: glutamic acid in the D-configuration"
; US-08-502-989-13

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Query Match          19.5%; Score 27.5; DB 1; Length 25;
Best Local Similarity 50.0%; Pred. No. 1.9e+03;
Matches 7; Conservative 1; Mismatches 5; Indels 1; Gaps 1;

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Qy 6 KPDEGKRGDACEGD 19
   :| | | | |
Db 3 RPKGXRGDXPXGD 15

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RESULT 15
US-08-502-989-20
; Sequence 20, Application US/08502989
; Patent No. 5681925
; GENERAL INFORMATION:
; APPLICANT: Broersma, Robert J
; APPLICANT: Owen, Thomas J
; APPLICANT: Krstenansky, John L
; TITLE OF INVENTION: TRIFUNCTIONAL ANTITHROMBIN AND
; TITLE OF INVENTION: ANTIFLATELET PEPTIDES
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merrell Dow Pharmaceuticals Inc.
; STREET: 2110 E. Galbraith Road, P.O. Box 156300
; CITY: Cincinnati
; STATE: Ohio
; COUNTRY: USA
; ZIP: 45215-6300
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/502.989
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/076,066
; FILING DATE: 11-JUN-1993

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; ATTORNEY/AGENT INFORMATION:
; NAME: Boudreaux, William R
; REGISTRATION NUMBER: 35,796
; REFERENCE/DOCKET NUMBER: MO1696 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 513/948-6586
; TELEFAX: 513/948-7961 or 4681
; TELEX: 214320
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "Xaa at location 1 is
; OTHER INFORMATION: phenylglycine in the D-configuration"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 6
; OTHER INFORMATION: /note= "Xaa at location 6 is D-Cys
; OTHER INFORMATION: sulfide bonded to D-Cys at location 13"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 11
; OTHER INFORMATION: /note= "Xaa at location 11 is
; OTHER INFORMATION: norleucine"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 13
; OTHER INFORMATION: /note= "Xaa at location 13 is D-Cys
; OTHER INFORMATION: sulfide bonded to D-Cys at location 6"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 24
; OTHER INFORMATION: /note= "Xaa at location 24 is
; OTHER INFORMATION: cyclohexylalanine"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 25
; OTHER INFORMATION: /note= "Xaa at location 25 is
; OTHER INFORMATION: glutamic acid in the D-configuration"
; US-08-502-989-20

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Query Match          19.5%; Score 27.5; DB 1; Length 25;
Best Local Similarity 50.0%; Pred. No. 1.9e+03;
Matches 7; Conservative 1; Mismatches 5; Indels 1; Gaps 1;

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Qy 6 KPDEGKRGDACEGD 19
   :| | | | |
Db 3 RPKGXRGDXPXGD 15

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Search completed: February 26, 2004, 09:50:42
Job time : 24 secs

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